

PD 09-APR-1998.
 XX
 PF 30-SEP-1997; 97WO-US17555.
 XX
 PR 30-SEP-1996; 96US-0026855.
 XX
 PA (EXSE-) EXSEED GENETICS LLC.
 XX
 PI Guan H, Keeling P;
 XX
 DR WPI; 1998-240100/21.
 XX
 DR P-PSDB; AAW56485.
 XX
 PT Hybrid polypeptide comprising starch-encapsulating region and
 PT protein - useful for, e.g. producing protein(s) resistant to
 PT degradation by stomach acids
 XX
 PS Example 2; Page 32-34; 156pp; English.
 XX
 CC The sequence is that of the waxy gene which codes for starch
 CC synthase. It can be used in the production of a hybrid
 CC polypeptide comprising a starch-encapsulating region (SER) fused
 CC to a payload protein. The hybrid polypeptide can be used to make
 CC modified starches comprising the payload protein, selected from,
 CC e.g. hormones, growth factors, antibodies, enzymes, dyes,
 CC immunoglobulins, etc. The modified starch can also be used
 CC to provide grain feeds enriched in amino acids. By encapsulating
 CC the payload protein in starch, it is more resistant to
 CC degradation by stomach acids.
 XX
 SQ Sequence 2542 BP; 610 A; 665 C; 693 G; 574 T; 0 other;
 Query Match 29.6%; Score 388.4; DB 19; Length 2542;
 Best Local Similarity 59.1%; Pred. No. 1.1e-56;
 Matches 795; Conservative 0; Mismatches 461; Indels 90; Gaps 4;

QY 5 TGGACATCGTGTGTTGCTGTAGTTCGCGCCCTTGTTCACAGAGCGCGCGCTGGGCG 64
 DB 700 TGAAGCTCGTGTGTCGCGCGCGAGATGGCCCTTGGAGCAAGACCGCGCGCTCGTG 759
 QY 65 ATGTGACTGTGGCTGCTATTGAGCTGTCAAGCGCGGCCACCGCTCATGACCATG 124
 DB 760 AGTCTCTGGTGGCTCCCTCCCTGCCATGGCTGCGNATGCCACAGGTCATGGTCACT 819
 QY 125 CCCCTCGTACGACAGTACGTGAGCGCTGGGACACCTCGGTGTGTCGATCATG 184
 DB 820 CTCTCTCGGTACGACAGTACAGGAGCGCTTGGATACCAAGCGTTGGCTGAGATCAAG 879
 QY 185 -----GCGAGAGTCCGCTACTTCCACTCCATCAAGAGGCGTGCACCGG 232
 DB 880 TTGCAACAGGTACGAGAGGTTGAGGTTTTTCCATTGTACAAAGCGTGGAGTCGACCGTG 939
 QY 233 TGTGGATTGACCAACCCCTGTTCTTGGCCCAAGCTCTGGGCAAGACCGGCTCCAACTGT 292
 DB 940 TGTTCATGACCATCGGTATTCCTTGGAGAAGTTTGGGGAAGACCGGTGAGAAGATCT 999
 QY 293 AGGCCCCCGCTCCGCGCTGACTACTGTGGAACAACCAAGCGCTTCGCCCTGTTCTGCA 352
 DB 1000 ACGGACCTGACACTGAGTGTATTACAAAGACAACAGATGGCTTTCAGCCCTCTTTGCC 1059
 QY 353 AGGCGCGTATTGAGGTGCGCGGCTGCTGCCCTTCGGCCCC----- 393
 DB 1060 AGGCGACTCGAGGCTCTAGATCTCTAAACCTCAACCAACCAACCACTACTTCAAGGAA 1119
 QY 394 -----GGCGAGACTCGCTTCTGCTGGGCAAGCAAGTACGCTCGCGCTGGCGCTGC 448
 DB 1120 CTTATGGTGAAGATGTTGTTCTGCTGCAAGCACTGGCACACTGCCCACTGGCAGCT 1179
 QY 449 TGTGAAGACGAGTACCAAGCCCAAGGCGAGTTCAACAAGGCGCAAGTGGTGGTGA 508
 DB 1180 ACCTGAAGAACAACATACCAAGCCCAATGGCATCTACAGGAATGCAAGGTTGCTTTCTGCA 1239
 QY 509 TCCACAACATCGCTTCCAGGGCGCGCATGTGGGAGGAGGCTTTCAGGAGACACGAACTGC 568

DB 1240 TCACAACATCTCTTACAGGGCGGCTTTCGCTTTTCAGGATTACCTCGAGCTGAACCTCT 1299
 QY 569 CCAGGCGCGCTTTGACAAGCTGGCGCTTCTCGGACGCGCTATGCCAAGTTTACACTGAGG 628
 DB 1300 CCGAGAGTTTCAGTCTATCTTCGATTTCATCAGCGGGTATGAC----- 1343
 QY 629 CCACCCCATGGAGGAGGACGAGAACCCCGCTGACGGGAAAGACTTACAAGAAGATCA 688
 DB 1344 -----ACGCGGTGGAGGACGAGGATCA 1368
 QY 689 ACTGGCTGAAGGTGGCAATTATCGCCCGGACAAAGCTGGTGTGACTGTGCGCCCACTAG 748
 DB 1369 ACTGATGAAGCGCGAATCTTGAAGCGGACAGGTGCTACCGTGAAGCCGCTACTAG 1428
 QY 749 CGACCCAGATCGTCCGATGCGCGCGGTGTGTGAGCTGGACCGCTCATCCGCGCA 808
 DB 1429 CGAGGAGCTCATCTCCGGATCGCCAGGGATCGGAGCTCGACACATCATCGCGCTCA 1488
 QY 809 AGGCAATTGAGGSCATTGTGAAGCGCATGACATTGAGGAGTGAACCCCAAGACGACA 868
 DB 1489 CCGCATACCGGSCATCGTCAACGGCATGACGTCAAGAGTGGGATCTTAGCAAGACA 1548
 QY 869 AGTTCGTGTGCGCCCTAGCACCAAGAGCTCTACGCCGCAAGGCGCGCCCAAG 928
 DB 1549 AGTACATCACCGCCAAAGTACGACGCAACCAACGCAATTCGAGGCGAAGGCGCTGAACAAG 1508
 QY 929 AGGCGCTGAGCGCGAGCTGGCGCTGCTGTGACCCCAACCGCCCTGTTTCGCGCTTCA 988
 DB 1609 AGCGTTGAGCGCGAGCGGGTCTTCCGGTGCAGAGGAATCCCACTGATCGCGTCA 1668
 QY 989 TCGGCGCTGAGGAGCAAGAGGTGTGACATCATCTTGGCGCGCCCTGCGCCCAAGATCC 1048
 DB 1669 TCGGAGGCTGAGGAAACAGAGGCGCTGACGTCTATGGCGCGCCATCCCGGAGCTCA 1728
 QY 1049 TGCCACCCCAAGTGCAGTCCCATCTGGTACCGCAAGCGCGCTTACGAGAAGC 1108
 DB 1729 TG---CAGGAGGACGTCCAGATCGTTCTTCTGGGTACTGGAAGAAGAGTTTCCGAAGC 1785
 QY 1109 TGTGAACGCTATCGGCACCAAGTACAAGGCGCGCCCAAGGCGGTGTTCAAGTTCTCGG 1168
 DB 1786 TGCTCAAGCATGAGGAGAGTATCTCCGGCAAGGTGAGGCGGTGGTGAAGTCAACG 1845
 QY 1169 CGCCCTGGGCAACATGCTCACCGCGCGCGCCGACATCATGCTGTGTCCTCGCGCTCG 1228
 DB 1846 CGCGCTTGTCTATCTCATCATGTCGCGGAGCGGACGTGTCGCGCTCCCGAGCGCTCG 1905
 QY 1229 AGCCTGCGGCTGATCCAGCTGCACGCCATGCATACGTACCGTACCGTCCCGTGTAGCCT 1288
 DB 1906 AGCCCTGTGACTCATCCAGCTCGAGGAGTACGATACGGAACGCCCTGTGCTTGCCTG 1965
 QY 1289 CCACCGCGGCGCTGTGTCGACACCGTC 1314
 DB 1966 CCACCGGTGGCTCGTGGACACCGTC 1991

RESULT 4
 ABK53210
 ID ABK53210 standard; DNA; 2161 BP.
 XX
 AC ABK53210;
 XX
 XX 14-AUG-2002 (first entry)
 XX
 DE Potato granule-bound starch synthase I (GBSSI) DNA sequence.
 XX
 KW Starch; amylose; cereal crop; commodity starch; thickened foodstuff;
 KW bread; baking; pasta; potato; granule-bound starch synthase I; GBSSI; ds.
 XX
 OS Solanum tuberosum.
 XX
 PN WO200218606-A1.
 XX

XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.


```
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match      20.6%; Score 271.2; DB 21; Length 2115;
Best Local Similarity 54.3%; Pred. No. 5,1e-37;
Matches 722; Conservative 0; Mismatches 518; Indels 90; Gaps 5;

QY 20 TTGCTGTGAGTCCGCCCTTGGTCCAAAGACGGCGGCTGGGCGATGTGATGGTGCC 79
DB 415 TTGGAGCTGAAGTTGGTCCATGGAGTAAACTGGTGGTCTTGGTGTGATGTTCTCGGTGTC 474

QY 80 TGCCTATTGAGCTGTCAAGCGCGCCACCGGTCATGACCATTCGCCCTCGCTACGACC 139
DB 475 TACCTCCAGCTCTGTCTGCTAGAGCCACCGGTGTGATGACAAATTTGCTCGGTATGACC 534

QY 140 AGTAGCTGACGCTGGGACACCTCGGTGGTCTGTCAGATCAAGTTGGGGATAAAGTTG 187
DB 535 AATATAAGATGCTTGGGACACTTGTGTGTGTTCAATCAAGTTGGGGATAAAGTTG 594

QY 188 AGAAGTCGGCTACTTCCACTCCATCAAGAAGGGCGTGCACCGGTGTGGATGTACACACC 247
DB 595 AGAATGTTCGTTTCTTCCATTGTACAAACGAGGAGTTGATCGTGTCTTTGTGGACCATC 654

QY 248 CCGTGTCTCGGCAAGTCTGGGCAAGACGGCTCCAAAGCTGACGGCCCGCCCTCGG 307
DB 655 CAATCTTCTTGTCTAAGTTGTGGCAAAACAGGATCCAAATCTATGTCCTATAACTG 714

QY 308 GCGTGTACTACTGGACACCAACCAAGCGCTTCCGCTGTCTGCAAGCGCGCTATTGAGG 367
DB 715 GAGTAGACTCAATGACACCAACCACTCCGTTGAGTTGTTGTGTGTCAGCTGCTCTTGAGG 774

QY 368 CTCGCCGGTCTGCGCTTCGGCCCGCGGAGGACTGC----- 405
DB 775 CACCACAGGTTCTGAACCTGAACAGCAGCAAGTACTTCTCTGGACCATATGTTGAGATG 834
```

```
QY 406 --GTCTTCGTGGCCAAAGCACTGGCACTCCGCCCTGTGGTCCCTCTCTGCTGAAGSACGAGT 463
DB 835 TAGTCTTTTGTGGCAATGACTGGCACACTGCTCTACTTCCATGTACTTCAATCTAATGT 894

QY 464 ACCAGCCCAAGGGCCAGTTCCACCAAGCCCAAGTCGGTGTGGCTATCCCAACATCCGCT 523
DB 895 ATCAATCCCGCGGAGTCTACATGAATGCAAAAGGTGCTTCTGCTCATTCACAACATAGCCT 954

QY 524 TCCAGGSCCGCATGTGGGAGGAGCTTCAAGACACAGCAAGCTGCCCGAGCGCCCTTG 583
DB 955 ACCAGGGAAGATTT-----GCCTTTG 975

QY 584 ACAAGCTGGCCTTCTCGGACGCTATGCCAAGGTTTACACTGAGCCACCCCATGAGG 643
DB 976 ATGACTATTCCCTTCTCAACTTGCCTCATGCTTTAAAGTCTTTCGACTTCATGAGC 1035

QY 644 AGGACGAGAAGCCCGCTGACGGGAAAGACCTTACAAAGATCAAACTGCTGAAAGGTTG 703
DB 1036 GGTATGAAAAGCC-----AGTAAAGGACGGAATAAATACTGGATGAAGGCTG 1083

QY 704 GCATTATCCCGCGGACAAAGCTGGTGAAGTGTGCGCCCACTACGCGACCGGATCGCTG 763
DB 1084 CAATTCTGGAAGCTACCGGTGCTTAAACAGTTAGTCCACTACTACGCTCAAGAACTCATCT 1143

QY 764 CCGATGCCCGCGGTGTGGAGCTGGACACCGCTCATCCGCGCAAGGGCATTGAGGGCA 823
DB 1144 CTGGAGTTGATAGAGCGTGGAAATTCATATAATCTTGAATGAAACAGTTTCCGGAA 1203

QY 824 TTGTGAACGGATGACATTTGAGAGTGGAAACCCCAAGACCGACAAAGTTCCTGTCTGCGC 883
DB 1204 TTATTAATGGAATGGATGTCAAGAAATGGAACCCGCTACTGACAAAGTACATGATATCA 1263

QY 884 CCTACGACCAGAACCGCTCTAGCCCGGCAAGCCCGCCAGGAGGCGCTCCAGGCGG 943
DB 1264 AATACGATATTACCCTGTACAGATGCTTAACCATTTGATCAAGAAGACACTTCAGGCTG 1323

QY 944 AGCTGGGCTGTGCTGTGGACCCACCGCCCTGTTCGCTTTCATCGGCGCGCTGGAGG 1003
DB 1324 CTGTTGGACTTCCCGTGGACAGGAGTCCCGGTATCGSTTTCATAGGAGATTGGAGG 1383

QY 1004 ASCAGAAGGTTGACATCATCTGGCGCGCCCTGCGCCAGCTTCCGCTTTCATCGGCGCGCTGGAGG 1063
DB 1384 ASCAGAAGGTTTCTGATATTTCTAGTGAAGACTATTTCCAAAGTTCATGG---GSCCTCAATG 1440

QY 1064 TGCACATCCCATCTGGGTACCGGCAAGCGCCCTTACGAGAAGCTGGTGAACGCATCG 1123
DB 1441 TTCAGATGGTTATCCCTGGGACTGGAAAGAAAGATGAGGCTCAGATCTTTGAACATG 1500

QY 1124 GCACCAAGTACAAAGGCGCGCCCAAGGGGTGGTCAAGTTCCTCGGCGCCCTGGCGCAC 1183
DB 1501 AAGAGAAGTTCACGGAAGGCGGTGGAGTGGCGAAATTCACGTCGCTTGGCTCAT 1560

QY 1184 TGCTCACCGCGCGCGGACCTTCATGCTGGTCCCTCGGCTTCGAGCCCTCGGCGCTGA 1243
DB 1561 TGATCAGCTGGAGCTGACCTCATTTGTCCTCCCAAGCAGGTTTGGCGGTGTGCTCTCA 1620

QY 1244 TCCAGCTCACGCCCATGCACTACGCTACCGTCCGCTGTGTGCTCCCTCCACCGCGCGCTGG 1303
DB 1621 TTCAGCTGCACGCAATGAGATGATGAACCGTCCCTATTTGTGTCATCTACTGTGGACTTG 1680

QY 1304 TGGACACCGT 1313
DB 1681 TGGACACTGT 1690
```

```
RESULT 6
ABK53215
ID ABK53215 standard; cdna; 2183 BP.
XX AC ABK53215;
XX DT 14-AUG-2002 (first entry)
```

XX Canna edulis granule-bound starch synthase I (GBSSI) cDNA sequence.
 DE Starch; amylose; cereal crop; commodity starch; thickened foodstuff;
 KW bread; baking; pasta; potato; granule-bound starch synthase I; GBSSI; ss.
 XX Canna edulis.
 XX WO200218606-A1.
 XX 07-MAR-2002.
 XX 28-AUG-2000; 2000WO-US23494.
 XX 28-AUG-2000; 2000WO-US23494.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Broglie K, Lightner J;
 XX WPI; 2002-404556/43.
 XX Novel starch isolated from cereal crop with a modification of amylose
 PT content and/or amylose weight distribution relative to commodity starch
 PT from same species of the cereal crop, for preparing thickened
 PT foodstuffs
 XX Example 1; Page 37-38; 44pp; English.
 XX The present invention relates to a new starch comprising amylose, 50%
 CC where the starch is isolated from a cereal crop, and comprises a
 CC increase in average molecular weight relative to commodity starch from
 CC the same species of the cereal crop from which starch was isolated.
 CC The starch of the invention is useful for preparing thickened foodstuffs
 CC by combining the starch, a foodstuff and water and cooking the resulting
 CC composition as necessary to produce a thickened foodstuff. The invention
 CC is also useful for preparing foodstuffs such as breads, baked goods,
 CC pastas, etc. The present nucleic acid sequence represents the Canna
 CC edulis granule-bound starch synthase I (GBSSI) cDNA sequence in clone
 CC ectlc.pk007.015 that was used in the methods of the invention for
 CC generation of a full-length sense Canna edulis GBSSI construct.
 XX Sequence 2183 BP; 636 A; 428 C; 516 G; 603 T; 0 other;
 SQ
 Query Match 16.5%; Score 217.2; DB 24; Length 2183;
 Best Local Similarity 51.1%; Pred. No. 5.9e-28;
 Matches 688; Conservative 0; Mismatches 568; Indels 90; Gaps 4;
 QY 5 TGCACATCGTATGGTGTGCTGAGTGGCGCCCTTGGTCCAGAGCGGCGCTGGGCG 64
 DB 357 TGAACCTGGGGTTTGTGTTGTGAGTGGTCCATGGAGCAAACTGGGGGCTTGGCG 416
 QY 65 ATGTGACTGGTGGCTGCTATTGAGTGGTCAAGCGGCGCCACGCGTCATGACCATG 124
 DB 417 ATGTTCTTATAGATTGCCACCTGTATGGTGGCAATTTGGGCACAGGGTCATGACCGTGG 476
 QY 125 CCCTCGCTACGACAGTACGCTGCGCTGGGACACCTCGGTGCTGCTGGACAT----- 179
 DB 477 CGCCAGATGACCAATATAAGATATCTGGATACAGTGTCCAGTTGAGTTAAAG 536
 QY 180 -----CATGGCGAGAAGGTCGGTACTTCCACTCCATCAGAGAGGCGGTGACCGCG 232
 DB 537 TTGGGATTAAGATTAAACTGTCCGTTCTTCCACTGCTACAAAGGGGAGTTGATCGGG 596
 QY 233 TGTGGATTACACACCCCTGCTTCCGCAAGTCTGGGCAAGACCGGCTCCAACTGT 292
 DB 597 TTTTGTGATCACCTATGTTTCTCGAGAAGTTTGGGGAAACAGAGGAAATAT 656
 QY 293 AGGGCCCCCGCTCCGCGCTGACTACCTGGACACCAACCAAGCGCTTTCGCCCTGTTCTGCA 352
 DB 657 ATGTTCTCTGTACAGGAACAGATTATGACAGCAATCAACTAAGATTACAGCTTTTGTGCC 716
 QY 353 AGGCCCTATTGAGGCTGCCCCGCTGCTGCCCTTCGGCCCC----- 393

DB 717 TGGCAGCTCTGGAAGCTCCAGACTTCTAAATCTCAACAACAGCAAAATCTATTCTGGAC 776
 QY 394 -----GGCGAGGACTGCTTCTCGTGGCGCAAGCTGGCACTCCGCGCTGGTGGCGTCC 448
 DB 777 CATATGGAGATGATGTTGTGTTTATGCAACAGATGGCATTTCTGCTACTGCGCTGCT 836
 QY 449 TGCTGAAGGACGAGTACCAAGCCCAAGGGCCAGTTTCAACAGCCCAAGTGGTGGTGA 508
 DB 837 ACTTCAAAACTATGTACCAATCACATGTTATTACATGAATGCTAAGGTTGATTTTGA 896
 QY 509 TCCACAACATCCCTTCCAGGCGCGCATGTGGAGGAGGCTTTCAGAGACAGAACTGC 568
 DB 897 TTCATAATATTGCTTACCAGGCGCGATTTCCTTTTCGAGCTTTGAATCTTAAATCTCC 956
 QY 569 CCCAGGCGCGCTTTCACAAGCTGGCTTCTCGAGGCGGTATGCCAAGGTTTACACTGAGG 628
 DB 957 CCAATAAATTTAAATCTTCAATTTGATTCATGATGATATGACAACT----- 1006
 QY 629 CCACCCCATGAGGAGGAGGAGAGAGAGCCCGCTGACGGGAAGAGCTTACAAGAGATCA 688
 DB 1007 -----GTGAAGGAAGGAAATAA 1025
 QY 689 AGTGGCTGAAGGTTGGCATTTATCGCGCGCAAGCTGGTGTGCTGCGCCCAACTAG 748
 DB 1026 ATTGGATGAAGGCTGGAATTAATAGAAATGTAGTGGTGTGACCGTGAGCCCATATATG 1085
 QY 749 CGACCGAGATCGTCCGATGCGCGCGGTGTGTCAGTGGACACCGCTCATCCCGCCA 808
 DB 1086 CCCAAGAGCTTGTCTCAGGGGTAGAGAAGGTTCTTCAGTTGGCAATATCTTCGCGCATGA 1145
 QY 809 AGGGCANTGAGGCGCATTTGAACGGCATGACATTCAGGAGTGGAAACCCCAAGACCGACA 868
 DB 1146 AAACCATCTGTGGAATAGTAAATGGGATGGACACACCGAGTGAATCTTAAACAGACA 1205
 QY 869 AGTTCCTGCTGCGCCCTAGCACCAGACAGGCTCTACCGSCAAGCGCGCGCAAGG 928
 DB 1206 AATATATTCTTCAAACTACGATGCAACACTGATTTGATGATGCAAAACCTCTCTGTAAG 1265
 QY 929 AGCGCCCTGAGGCGCGAGCTGGGCTGCTGTTGGACCCCAACCGCCCTGTTTCGCCCTTCA 988
 DB 1266 AAGCTTTGCAAGCTGAGTGGGCTGCTTAAACAAAACAAAGCTTGTTCGCCCTTG 1325
 QY 989 TGGCGCGCTGAGGAGACAGAGGTTGTGACATATCTTCGCGCGCTGCGCCCAAGATCC 1048
 DB 1326 TTGGAAGACTAGATGACAGAGAGGCTCAGACATTTAGCTGCAGCAATTCAGAGACTTC 1385
 QY 1049 TGGCCACCCCAAGGTGCAGATCGCCATCTGCTGGTACCGGCAAGCGCGCTACGAGAAGC 1108
 DB 1386 TTGTGAG---AATGTTCAAGTGAATGATGCTGGGCACTGGCAACAGAGTTGGAGAGTG 1442
 QY 1109 TGGTGAACGCCATCGGCACCAAGTACAGGGCGCGCGCAAGGCGGTGGTCAAGTTCTCGG 1168
 DB 1443 AACTTACATTTACTTGAAGAAATGTTTCCAGACAAATTCAGAGCACATCTCAAAATCAACG 1502
 QY 1169 CGCCCTGGGCGACATGCTCACCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1228
 DB 1503 TTCCCTTAGCTCATGCAATCATGGCAGAGCTGATATCTTGTATTTCCAAGCAGATTCG 1562
 QY 1229 AGCCCTGGCGCTGATCCAGCTGCACGCCATGCACTACGCTACCGTGGCGGTGGTACGCT 1288
 DB 1563 AACCTTGTGGCTCATTCAGCTTCAGGCCCATGGCATATGGAACCTCCCTATGTTAGCA 1622
 QY 1289 CCACCGCGCGCTTGGTGCACACCGTC 1314
 DB 1623 CCACCTGTTGACTTGTGACACTGTC 1648

RESULT 7
 AAC86435
 ID AAC86435 standard; cdna; 2807 bp.
 XX
 AC AAC86435;

QY 533 GCATGTGGAGGAGGCTTTCAAGACACGAGCTGCCAGCGCGCTTTGACAAAGCTGG 592
Db GTGGCCCTGTAGATGAATCCCGTTCCAGCTGCTGAGCAGTACCTGGAACACTTCA 1668
QY 593 CTTCTTCGACGCTATGCCAAGGTTTACTACTGAGGCCACCCCATGAGGAGGACGAGA 652
Db GACTGTACGACCCCGTGGTGTGAACACCCCACTACTTCGCCCGCGGCTGAAGATGG 1728
QY 653 AGCCCCCGCTGACGGGAAGACCTACAAGAAGATCACTGCTGAAGGGTGGCATATCG 712
Db CGGACAGGTTGCTGTGTAGCCCGGCTACCTGTGGAGCTGAAGACGCTGGAGGGCG 1788
QY 713 CGCCGACAGCTGTGACTGTGTCCGCCCAACTACCGACCGAGATCGCTGCGCATGCCG 772
Db GCTGGGGGCTTACGACATCATACGCGACAGACACTGGA-----1827
QY 773 CGGGCGGTGTGGAGCTGACACCGCTCATCCGCGCCCAAGGCAATGAGGCAATGTGAACG 832
Db -----AGACCCCGCGCATGCTCAACGGCATCGCAACATGAGTGAACCCCGAGG 1878
QY 833 GCATGACATTTAGGAGTGGAAACCCCAAGACCGACAAAGTTCCTGTCTGGCGCTACGACC 892
Db TGGACGCCACCTCAAGTGGAGCGGTACACCAACTTCTCCCTGAGGACGC-----1929
QY 893 AGAACAGCTCTACGCGCGCAAGCGCGCCCAAGAGGCGCTTGCAGCGCGAGCTGGCG 952
Db -----TGGACTCGGCAAGCGGCACTGCAAGGAGGCGCTGACGCGGAGCTGGCG 1980
QY 953 TGCCTGTGAGACCCACCGCGCCCTGTTCGCTTATCGCGCGCGCTGGAGGAGGAGG 1012
Db TGCAGTTCGCGCGGACGCGCGCTGCTCGGCTTATCGCGCGCGCTGGAGGAGGAGG 2040
QY 1013 GTGTGACATCTCTGCGCGCGCTTGCACCAAGATCTGSCCAACCCCAAGGTGCATCG 1072
Db GGTGTGAGATCATCGGAGCGCATGCTGCTGATCGT---AGCCAGGACGTGCAGCTGG 2097
QY 1073 CCATCTGTGATACGGGAGCGCGCTACGAGAAGCTGTGAACGCCATCGGCACCAAGT 1132
Db TGATCTGGACCGCGCGCGCACGACCTGGAGAGCATGCTGACACATTCGAGCGGGAGC 2157
QY 1133 ACAAGGCGCGCGCAAGGCGGTGTCAAGTTCGCGCGCGCTGCGGCGCGCTGCGGCGCG 1192
Db ACCAGCAAGGTGCGCGGCTGCGGCGCGCTGCGGCGCGCTGCGGCGCGCTGCGGCGCG 2217
QY 1193 CCGGCGCGGACTTCATGCTGTGCTGCTGCGCTTGCAGCGCTGCGGCGCGCTGCGGCGCG 1252
Db CGGCGCGGACGCGCTCTCATGCGCTCCCGCTGCGGCGCGCTGCGGCGCGCTGCGGCGCG 2277
QY 1253 AGCCATGCACTACGATACCGTACCGTGTGCTGAGCTTCCACCGCGCGCGCTGCGGCGCG 1312
Db ACGCATGGCTACGGCACCGCTGCCGCTGCTGACGCGCGCTGCGGCGCGCTGCGGCGCG 2337
QY 1313 T 1313
Db 2338 T 2338

RESULT 10
ID AAV66834 standard; DNA; 2380 BP.
XX AAV66834;
AC AAV66834;
XX
DT 05-JAN-1999 (first entry)
XX Zea mays soluble starch synthase gene SSS56.
DE Zea mays; US yellow-dent corn line; maize; soluble starch synthase;
KW SSS; glycogen biosynthetic pathway; branching enzyme; ss.
XX Zea mays.
XX US5824790-A.

XX 20-OCT-1998.
XX 15-DEC-1995; 95US-0572951.
XX 15-DEC-1995; 95US-0572951.
PR 21-JUN-1994; 94US-0263921.
PR 29-NOV-1994; 94US-0346602.
XX (ZENE) ZENCA LTD.
XX Guan H, Keeling PL, Knight ME;
PI WPI; 1998-582626/49.
DR
XX Isolated nucleic acid molecule, used to produce transgenic plants -
PT comprises nucleotide sequence encoding polypeptide having soluble
PT starch synthase activity, where polypeptide is encoded by maize gene
XX
PS Claim 3; Column 31-33; 29pp; English.
CC The present sequence represents an isolated nucleic acid molecule which
CC has been isolated and comprises a nucleotide sequence encoding a
CC polypeptide having soluble starch synthase (SSS) activity, where the
CC polypeptide is encoded by a maize gene. The isolated nucleic acid
CC molecule can be used to produce transgenic plants with altered starch
CC production. The transgenic plants produced using the nucleic acid
CC molecule have an enhanced ability to produce structurally-altered starch.
XX
SQ Sequence 2380 BP; 333 A; 266 C; 518 G; 272 T; 991 other;
Query Match 15.2%; Score 199.6; DB 19; Length 2380;
Best Local Similarity 35.0%; Pred. No. 5.3e-25;
Matches 463; Conservative 183; Mismatches 594; Indels 84; Gaps 6;
QY 5 TGGACATGCTGATGTTGCTGCTGAGTGCCTTGGTCCCAAGCGCGCGCTTGGGCG 64
Db 677 TGAAYTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNGTNG 736
QY 65 ATGTGACTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
Db 737 ATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796
QY 125 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 184
Db 797 THCCNMGNATAYGNGARTAYGNGARTAYGNGARTAYGNGARTAYGNGARTAYGNGART 854
QY 185 GCGAAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
Db 855 RTGTCG 913
QY 245 ACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
Db 914 TGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 973
QY 305 CGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 364
Db 974 GNYTNGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1033
QY 365 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
Db 1034 AYGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1093
QY 425 GCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 484
Db 1094 GCGAAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1153
QY 485 CCAAGGCG 544
Db 1154 ARTAGCNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNG 1213
QY 545 AGGCTTCAAGGACACGAGCTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 604

Job time : 232.966 secs

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 09:33:29 ; Search time 1282.02 Seconds
(without alignments)
16599.542 Million cell updates/sec

Title: US-09-980-771A-6

Perfect score: 1314

Sequence: 1 gcactgacatcgtgatggt.....gcggcctggtcacacgctc 1314

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estiba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_esti:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_roo:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469.8	35.8	473	10	AV640741
2	457.8	34.8	461	10	AV629488
3	444.4	33.8	458	10	AV622787
4	400.8	30.5	436	10	AV629117
5	395.6	30.1	511	10	AV394077
6	384.6	29.3	2147	11	AY109531

7	365.2	27.8	475	10	AW757933
8	337.8	25.7	418	10	AV644765
9	295.8	22.5	506	10	AV643281
10	278.4	21.2	702	14	BQ246353
11	272.8	20.8	560	10	AV628313
12	251.8	19.0	552	10	BE024926
13	250.2	19.2	517	10	AV641583
14	245.6	18.7	726	14	BQ804991
15	244.2	18.6	532	10	AV641989
16	235.8	17.9	513	10	AV631004
17	235.8	17.9	552	10	AV640546
18	234.8	17.9	524	10	AV641724
19	234.2	17.8	500	10	AV642869
20	231.8	17.6	510	10	AV395307
21	223.8	17.0	540	10	AV642722
22	211.8	16.1	486	10	AV642834
23	211.8	16.1	504	10	AV629198
24	210.8	16.0	502	10	AV644517
25	208.8	15.9	495	10	AV642565
26	207.8	15.8	696	12	BG351920
27	207	15.8	641	14	BQ247154
28	206.8	15.7	522	10	BE423625
29	206.4	15.7	729	12	BG599615
30	201.2	15.3	585	14	BQ246366
31	200.8	15.3	493	10	AV631838
32	199.8	15.2	492	10	AV629891
33	198.8	15.1	484	10	AV629266
34	198.8	15.1	489	10	AV629190
35	196.8	15.0	773	12	BG351175
36	196.2	14.9	734	12	BG350240
37	193.8	14.7	487	10	AV643763
38	193.6	14.7	385	10	AV393664
39	193.6	14.7	436	14	BQ245102
40	189.8	14.4	541	10	BE424431
41	189.8	14.4	631	13	BF531619
42	188.8	14.4	490	10	AV628140
43	187.8	14.3	476	10	AV644278
44	185.8	14.1	478	10	AW758015
45	185.8	14.1	502	10	AV631098

ALIGNMENTS

RESULT 1
AV640741
LOCUS AV640741 473 bp mRNA linear EST 15-DEC-2000
DEFINITION AV640741 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
cdna clone HCL021f06_r 5', mRNA sequence.
ACCESSION AV640741
VERSION AV640741.1 GI:10784069
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
AUTHORS Asamizu, E., Miura, K., Kuchio, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1..473
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"

```
/clone="HCL021f06_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/notes="Vector: pBluescriptII SK-; Site.1: EcoRI; Site.2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
BASE COUNT      76 a  162 c  146 g   89 t
ORIGIN

Query Match      35.8%; Score 469.8; DB 10; Length 473;
Best Local Similarity 99.6%; Pred. No. 3.8e-81;
Matches 471; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 TGGTTGCTGCTGAGTGGCCCTTGTCCTCAAGAGCGGCGCTGATGACTGGTG 76
Db 1 TGGTTGCTGCTGAGTGGCCCTTGTCCTCAAGAGCGGCGCTGATGACTGGTG 60
QY 77 GCCTGCTATTGAGTGGTCAAGCGGCGCCACCGCGTCATGACCATTCGCCCTGCTACG 136
Db 61 GCCTGCTATTGAGTGGTCAAGCGGCGCCACCGCGTCATGACCATTCGCCCTGCTACG 120
QY 137 ACCAGTACGCTGACGCTGGGACACCTCGGTGTCGTGGACATCATGGGCGAGAGTCC 196
Db 121 ACCAGTACGCTGACGCTGGGACACCTCGGTGTCGTGGACATCATGGGCGAGAGTCC 180
QY 197 GCTACTTCCACTCCATCAAGAAGGGGCTGACCGCGTGTGGATTGACCAACCCCTGTTCC 256
Db 181 GCTACTTCCACTCCATCAAGAAGGGGCTGACCGCGTGTGGATTGACCAACCCCTGTTCC 240
QY 257 TGGCCAGGCTTGGGCAAGACCGGCTCCAAAGCTGTACGCGCCCGCTCGGCGCTACT 316
Db 241 TGGCCAGGCTTGGGCAAGACCGGCTCCAAAGCTGTACGCGCCCGCTCGGCGCTACT 300
QY 317 ACCTGGCAACCAACAGCGCTGCGCCCTGTTCTGCAAGGCGCGTATTGAGGCTGCCCGCG 376
Db 301 ACCTGGCAACCAACAGCGCTGCGCCCTGTTCTGCAAGGCGCGTATTGAGGCTGCCCGCG 360
QY 377 TGTGTCCTTCGCGCCCGCGGAGACTGTGCTTCTGTTGGCGCAAGCTGGCACTTCGCGCC 436
Db 361 TGTGTCCTTCGCGCCCGCGGAGACTGTGCTTCTGTTGGCGCAAGCTGGCACTTCGCGCC 420
QY 437 TGTGTCCTTCGCTGCTGAAGGAGAGTACCAAGCCCAAGGCGCGTTCACCAAG 489
Db 421 TGTGTCCTTCGCTGCTGAAGGAGAGTACCAAGCCCAAGGCGCGTTCACCAAG 473

RESULT 2
AV629488
LOCUS
DEFINITION AV629488 Chlamydomonas reinhardtii 5% to 0.04% CO2 linear EST 15-DEC-2000
reinhartii cDNA clone LCL059f09_r 5', mRNA sequence.
ACCESSION AV629488
VERSION
KEYWORDS
SOURCE
ORGANISM
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE
AUTHORS Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
JOURNAL
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
1. .461
/organism="Chlamydomonas reinhardtii"

/strain="c9"
/db_xref="taxon:3055"
/clone="LCL059f09_r"
/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/notes="Vector: pBluescriptII SK-; Site.1: EcoRI; Site.2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
BASE COUNT      73 a  156 c  143 g   89 t
ORIGIN

Query Match      34.8%; Score 457.8; DB 10; Length 461;
Best Local Similarity 99.6%; Pred. No. 7.8e-79;
Matches 459; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ACATCGTATGCTGCTGAGTGGCCCTTGCTCAAGACGCGGCGCTGGGCGGATG 67
Db 1 ACATCGTATGCTGCTGAGTGGCCCTTGCTCAAGACGCGGCGCTGGGCGGATG 60
QY 68 TGACTGTTGGCTGCTTATGAGCTGCTCAAGCGCGGCCACCGGCTCATGACCATTCGCC 127
Db 61 TGACTGTTGGCTGCTTATGAGCTGCTCAAGCGCGGCCACCGGCTCATGACCATTCGCC 120
QY 128 CTCCTAGGACCATGAGCTGACGCTGGGACACCTCGGTGGTGGTGGACATGAGCGC 187
Db 121 CTCCTAGGACCATGAGCTGACGCTGGGACACCTCGGTGGTGGTGGACATGAGCGC 180
QY 188 AGAAGTCCGCTACTTCCACTCCATCAAGAAGGGGCTGACCGGCTGTGGATTGACCAAC 247
Db 181 AGAAGTCCGCTACTTCCACTCCATCAAGAAGGGGCTGACCGGCTGTGGATTGACCAAC 240
QY 248 CCTGTTCTCTGCGCAAGGCTTGGGCGCAAGACCGGCTCAAGCTGTACGCGCCCGCTCCG 307
Db 241 CCTGTTCTCTGCGCAAGGCTTGGGCGCAAGACCGGCTCAAGCTGTACGCGCCCGCTCCG 300
QY 308 GCGTGACTACTGACCAACCAACAGCGCTTCGCCCTTCTGCAAGGCGCGCTATTGAGG 367
Db 301 GCGTGACTACTGACCAACCAACAGCGCTTCGCCCTTCTGCAAGGCGCGCTATTGAGG 360
QY 368 CTGCGCGGCTGCTGCGCTTCGCGCCCGCGGAGGAGTGTGCTTGTGCGCAACGACTGGC 427
Db 361 CTGCGCGGCTGCTGCGCTTCGCGCCCGCGGAGGAGTGTGCTTGTGCGCAACGACTGGC 420
QY 428 ACTCGCGCTGCTGCGCTTCCTGCTGTAAGGAGGAGTACAG 468
Db 421 ACTCGCGCTGCTGCGCTTCCTGCTGTAAGGAGGAGTACAG 461

RESULT 3
AV622787
LOCUS
DEFINITION AV622787 Chlamydomonas reinhardtii 5% to 0.04% CO2 linear EST 15-DEC-2000
reinhartii cDNA clone LCL054e04_r 5', mRNA sequence.
ACCESSION AV622787
VERSION
KEYWORDS
SOURCE
ORGANISM
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE
AUTHORS Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
JOURNAL
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
```


Db 959 CCGAGGAGCTCATCTCCGGCATCCAGGGGCTCGAGCTCGACAAACATCATGCGCCCTCA 1018

QY 809 AGGCATTTAGGCGATTTGTGAACGGCATGGACATTTGAGGATGGAAACCCCAAGACCGGACA 868

Db 1019 CCGGCATCACCGGCGATGTCACAGGCGATGGAGCTCAGCGAGTGGAGCCCGACGAGGACA 1078

QY 869 AGTTCTCTGTGGCCCTAGCAGCAGACAGCGCTCTACGCGGCAAGCCCGCCCAAGG 928

Db 1079 AGTACATCGCGGTGAGTACACGTGTCGAGCGCGGTGGAGGCGCAAGCGGTGAACAAG 1138

QY 929 AGGCCCTGACAGGCGGAGCTGGCGCTGCTGTGACCCCGACCGCCCGCTGTTCGCCCTTCA 988

Db 1139 AGCGCTGACAGGCGGAGTCCGGCTCCCGTGGACCGGAACATCCCGCTGGTGGCGTTCA 1198

QY 989 TCGCGCCCTGGAGGAGCAGAGGCTGGACATCATCTCTGGCGCGCCCTGCCCCAAGATCC 1048

Db 1199 TCGCGAGGCTGGAGAGCAGAGGCGCCCGACGTCATCTGGCGCGCCCGACGCTCCCGAGCTCA 1258

QY 1049 TGGCCACCCCGCAAG--GTGCAGATGCCATCTCTGGGTACCGGCAAGCGCGCTTACGAGA 1105

Db 1259 TGGAGATGGTGGAGGAGTGCAGATCTTCTGTGGCGACGGGCAAGAGTTCGAGC 1318

QY 1106 AGCTGTGAACGCATCGGCACCAAGTACAAAGGCGCGCGCAAGGCGGTGTCAAGTTCT 1165

Db 1319 GCATGTCTATGAGCGCGAGGAGAGTTCGCCAGGCAAGTGGCGCGGTGTCAAGTTCA 1378

QY 1166 CGCGCGCCCTGGCGCATCTCACCGCGCGCGCGCTTCACTGTGTGCGCTTCGCGCT 1225

Db 1379 ACGGCGCTGGCGCACCATCATGCGCGCGCGCGAGCTGCTCGCGCTCACGAGCGCT 1438

QY 1226 TCGAGCCCTCGCGCTCATCGCTGACCGCCATGCTACGCTACGCTACGCTGCGCTGTAG 1285

Db 1439 TCGAGCCCTCGCGCTCATCGCTGACGCGGATGCGATACGGAACCGCTGCGCTGCG 1498

QY 1286 CTTCCAGCGCGCGCTGTGTGCGACCGCTC 1314

Db 1499 CGTCCACCGGTGACTGCTGCGACCATC 1527

RESULT 7
AW57933
LOCUS 874004E12.y1 C. reinhardtii CC-1690, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
DEFINITION
ACCESSION AW57933
VERSION AW57933.1 GI:7687285
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 475)
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P., McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers 1. .475
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: ECORI; Site_2: XhoI; This library, constructed by John Davies and Jeffrey

McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage."

BASE COUNT 74 a 160 c 143 g 98 t
ORIGIN

Query Match 27.8%; Score 365.2; DB 10; Length 475;
Best Local Similarity 97.9%; Pred. No. 6.5e-61;
Matches 370; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 CGCTGGACATCGTATGCTGCTGAGGTGCGCCCTTGTGTCACAGACGGCGGCTGG 61

Db 98 CGCTGGACATCGTATGCTGCTGAGGTGCGCCCTTGTGTCACAGACGGCGGCTGG 157

QY 62 GCGATGTGACTGTGGCTGCTGCTATTGAGCTGGTCAAGCGCGCCACCGCTCATGACCA 121

Db 158 GCGATGTGACTGTGGCTGCTGCTATTGAGCTGGTCAAGCGCGCCACCGCTCATGACCA 217

QY 122 TTGCCCCCTGCTACGACAGTACCTGACGCTGGGACACCTCGGTGCTGTGGACATCA 181

Db 218 TTGCCCCCTGCTACGACAGTACCTGACGCTGGGACACCTCGGTGCTGTGGACATCA 277

QY 182 TGGCGGAGAGTCCGCTACTTCCACTCCATCAAGAGGGGCTGCACCGCTGTGGATTG 241

Db 278 TGGCGGAGAGTCCGCTACTTCCACTCCATCAAGAGGGGCTGCACCGCTGTGGATTG 337

QY 242 ACCACCCCTGCTTCTGCGCAAGTCTGGGCAAGACCGGCTCCCAAGCTGTACGCGCCCC 301

Db 338 ACCACCCCTGCTTCTGCGCAAGTCTGGGCTAGACCGGCTCCCAAGCTGTACGCGCCCC 397

QY 302 GTCGCGCGCTGACTACTGAGCAACCAACAGCGCTTGCCTCTTCTGCAAGCGCGCTA 361

Db 398 GTCGCGCGCTGACTACTGAGCAACCAACAGCGCTTGCCTCTTCTGCAAGCGCGCTA 457

QY 362 TTGAGGCTGCCCGCTGC 379

Db 458 TTGAGGCTGCCCGCTGC 475

RESULT 8
AW644765
LOCUS AV644765
DEFINITION cDNA clone HCL093d12_r 5', mRNA sequence.
ACCESSION AV644765
VERSION AV644765.1 GI:10788093
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 418)
AUTHORS Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K., Nakamura,Y. and Tabata,S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yakusa 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp; URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers 1. .418
/organism="Chlamydomonas reinhardtii"


```
Query Match 21.2%; Score 278.4; DB 14; Length 702;
Best Local Similarity 66.3%; Pred. No. 4.3e-44;
Matches 399; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

QY 682 AAGATCAACTGGCTGAAGGTGGCTATTCGCGCCGACAGCTGGTGGTGTGTCGCC 741
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 103 AAGATCAACTGGATGAAGCGCGGATCTCGAGGCCGACAGGTGCTGAGGTGAGCC 162
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 742 AACTAGCGACCGAGATGCTGCGGATGCGCGCGCGGTGTGGAGCTGGACACCGTCATC 801
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 163 TACTAGCGGAGGAGCTCATCTCTGGGGAAGCCAGGGGCTGCGAGCTCGACATCATG 222
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 802 CGGCGCAAGGCGATGAGGCGATGTCAACGGCATGACATTTAGGAGTGAACCCCAAG 861
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 CGCTCACTGGGATCACCGCATCTGTCACGGGATGATGTAGCGAGTGGGACCCACC 282
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 862 ACGGACAAGTTCCTGTCTGCGCCCTACGACGACAGACGCTCTACGCGCAAGCGCCGC 921
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 283 AAGGACAAGTTCCTGCGCGTCACTAGACATCACACCGCTTGGAGGGAAGCGCGTG 342
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 922 GCGAAGAGCGCTGAGCGCGAGCTGGGCTGCTGTGTGACCCCGCCCGCTGTC 981
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 343 AACAAAGAGCGCTGAGCGCGAGTGGGCTGCGGTGACCGGAAGGTGCCCTGGTG 402
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 982 GCCTTCATCGCGCGCTGAGGAGGACGAAGGGTGTGGACATCATCTTGGCGCGCCGTC 1041
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 403 CGCTTCATCGCGAGCTGAGGAGGACGAAGGGCGCCGACGATGATGTCGCGGCAAC 462
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1042 AAGATCCTGCGCCACCCCAAGTSCAGATCGCATCTCGGTACCGGCAAGCGCGCTAC 1101
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 463 GAGATCCTGAAGGAGGAGCGTCCAGATGCTTCTCTGCGCACCGGGAAGAGAGTTC 522
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1102 GAGAAGCTGTTGAAGCGCATGCGCACAGTACAAGGCGCGCGCCAGGCGTGTCAAG 1161
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 523 GAGCGGCTACTAAGAGCAATTTAGAGGAAATCCCGAGCAAGGTGAGGCGCGTGTGAG 582
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1162 TTCTCGCGCGCCCTGGCGACATGCTCACCGCGCGCGCGACATCTGCTGTGCGCTCG 1221
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 583 TTCAAGCGCGCGTGGCTACACAGATGATGCGCGCGCGCGACGTCGCGCTACACAGC 642
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1222 CGCTTCAGCGCTGCGCGCTGATCCAGCTGACGCGCATGACGATACGCTGCGCGTG 1281
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 643 CGCTTCAGCGCTGCGCGCTCATCCAGCTCCAGGAGTGGCTACGGAAGCGCGTGGCG 702
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
AV628313
LOCUS
DEFINITION
AV628313 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas
reinhardtii cDNA clone LCL039h11_r 5', mRNA sequence.
ACCESSION
AV628313
VERSION
AV628313.1 GI:10790947
KEYWORDS
EST.
SOURCE
Chlamydomonas reinhardtii.
ORGANISM
Chlamydomonas reinhardtii.
Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE
1 (bases 1 to 560)
Asanizu,E., Miura,K., Kuchro,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y., and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
20539644
Contact: Erika Asanizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asanizukazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1..560
/organism="Chlamydomonas reinhardtii"

Query Match 20.8%; Score 272.8; DB 10; Length 560;
Best Local Similarity 99.3%; Pred. No. 5e-43;
Matches 274; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGCTGACATCGTGGTGTGCTGAGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTG 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 285 GCGCTGACATCGTGGTGTGCTGAGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTG 344
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 GCGATGTGACTGTGGCTGCCCTATTGAGCTGTCAAGCGCGCCACCGGCTCATGACC 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 345 GCGATGTGACTGTGGCTGCCCTATTGAGCTGTCAAGCGCGCCACCGGCTCATGACC 404
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 ATTGCCCTCGCTACGACCATGCTGAGCTGTGGACACCTCGTGTGTGGACATC 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 405 ATTGCCCTCGCTACGACCATGCTGAGCTGTGGACACCTCGTGTGTGGACATC 464
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 ATGGCGGAGAGGTCCTGCTGCTGCGCAAGTGTGGGCAAG 276
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 465 ATGGCGGAGAGGTCCTGCTGCTGCGCAAGTGTGGGCAAG 560
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 GACCACCCCTGCTTCTGCGCAAGTGTGGGCAAG 276
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 525 GACCACCCCTGCTTCTGCGCAAGTGTGGGCAAG 560
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
BE024926
LOCUS
DEFINITION
894006H08.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION
BE024926
VERSION
BE024926.1 GI:8287367
KEYWORDS
EST.
SOURCE
Chlamydomonas reinhardtii.
ORGANISM
Chlamydomonas reinhardtii.
Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE
1 (bases 1 to 552)
Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; Project phase 2
Unpublished (2000)
Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
Email: chlamy@duke.edu.
Location/Qualifiers
1..552
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 2lgr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/Note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
```

mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO₂ and HS medium bubbled with 5% CO₂. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."

```

BASE COUNT      91 a  185 c  167 g  109 t
ORIGIN

Query Match      19.2%; Score 251.8; DB 10; Length 552;
Best Local Similarity 99.2%; Pred. No. 5.8e-39;
Matches 253; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCCTGGACATCGTGTGCTGCTGAGGTGCGCCCTTGGTCCCAAGACGGCGGCTG 60
Db 298 GGCCTGGACATCGTGTGCTGCTGAGGTGCGCCCTTGGTCCCAAGACGGCGGCTG 357
QY 61 GCGATGTGACTGCTGCTGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 120
Db 358 GCGATGTGACTGCTGCTGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 417
QY 121 ATTGCCCTCGCTACGACAGTACGCTGAGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 180
Db 418 ATTGCCCTCGCTACGACAGTACGCTGAGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 477
QY 181 ATGGCGGAGAGTTCGGCTGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 240
Db 478 ATGGCGGAGAGTTCGGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 537
QY 241 GACCAACCCCTGGTTC 255
Db 538 GACCAACCCCTGGTTC 552

RESULT 13
AV641583
LOCUS      AV641583      517 bp      mRNA      linear      EST 15-DEC-2000
DEFINITION Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
cDNA clone HCL036908_r 5', mRNA sequence.
ACCESSION AV641583
VERSION   AV641583.1 GI:10784911
KEYWORDS  EST.
SOURCE    Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 517)
AUTHORS   Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
TITLE     Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL   DNA Res. 7 (5), 305-307 (2000)
MEDLINE   20539644
COMMENT   Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. .517
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="HCL036908_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"

BASE COUNT      91 a  185 c  167 g  109 t
ORIGIN

Query Match      19.2%; Score 251.8; DB 10; Length 552;
Best Local Similarity 99.2%; Pred. No. 5.8e-39;
Matches 253; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGCCTGGACATCGTGTGCTGCTGAGGTGCGCCCTTGGTCCCAAGACGGCGGCTG 60
Db 298 GGCCTGGACATCGTGTGCTGCTGAGGTGCGCCCTTGGTCCCAAGACGGCGGCTG 357
QY 61 GCGATGTGACTGCTGCTGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 120
Db 358 GCGATGTGACTGCTGCTGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 417
QY 121 ATTGCCCTCGCTACGACAGTACGCTGAGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 180
Db 418 ATTGCCCTCGCTACGACAGTACGCTGAGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 477
QY 181 ATGGCGGAGAGTTCGGCTGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 240
Db 478 ATGGCGGAGAGTTCGGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 537
QY 241 GACCAACCCCTGGTTC 255
Db 538 GACCAACCCCTGGTTC 552

RESULT 13
AV641583
LOCUS      AV641583      517 bp      mRNA      linear      EST 15-DEC-2000
DEFINITION Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
cDNA clone HCL036908_r 5', mRNA sequence.
ACCESSION AV641583
VERSION   AV641583.1 GI:10784911
KEYWORDS  EST.
SOURCE    Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 517)
AUTHORS   Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
TITLE     Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL   DNA Res. 7 (5), 305-307 (2000)
MEDLINE   20539644
COMMENT   Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. .517
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="HCL036908_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"

```

```

BASE COUNT      82 a  176 c  159 g  100 t
ORIGIN

Query Match      19.0%; Score 250.2; DB 10; Length 517;
Best Local Similarity 98.8%; Pred. No. 1.2e-38;
Matches 252; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTGGACATCGTGTGCTGCTGAGTGTGCGCCCTTGGTCCCAAGACGGCGGCTG 60
Db 263 GCCTGGACATCGTGTGCTGCTGAGTGTGCGCCCTTGGTCCCAAGACGGCGGCTG 322
QY 61 GCGATGTGACTGCTGCTGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 120
Db 323 GCGATGTGACTGCTGCTGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 382
QY 121 ATTGCCCTCGCTACGACAGTACGCTGAGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 180
Db 383 ATTGCCCTCGCTACGACAGTACGCTGAGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 442
QY 181 ATGGCGGAGAGTTCGGCTGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 240
Db 443 ATGGCGGAGAGTTCGGCTGCTGAGTGTCAAGCGCGCCACCGCGTCATGACC 502
QY 241 GACCAACCCCTGGTTC 255
Db 503 GACCAACCCCTGGTTC 517

RESULT 14
BQ804991
LOCUS      BQ804991      726 bp      mRNA      linear      EST 31-JUL-2002
DEFINITION whe3561_E02_J032s Wheat developing grains cDNA library Triticum
aestivum cDNA clone whe3561_E02_J03, mRNA sequence.
ACCESSION BQ804991
VERSION   BQ804991.1 GI:22029200
KEYWORDS  EST.
SOURCE    Bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 726)
Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J., Cronin
,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J.,
Wilson,C. and Woo,J.
The structure and function of the expressed portion of the wheat
genomes - Developing grains cDNA library
Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
Location/Qualifiers
1. .726
/organism="Triticum aestivum"
/cultivar="Butte 86"
/db_xref="taxon:4565"
/clone="WHE3561_E02_J03"
/clone_lib="Wheat developing grains cDNA library"
/tissue_type="whole grains"
/dev_stage="3-44 days post anthesis seed"
/lab_host="E. coli SOLR"
/note="Vector: Lambda ZAP II, excised phagemid; Site 1:
EcoRI; Plants were grown under six following different
environmental regimes in greenhouse, Environment 1)
24oc/17oc day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 24oc/17oc day/night,

```

well-watered, without post-anthesis fertilizer, Environment 3) 370c/170c day/night, well-watered, with post-anthesis fertilizer, Environment 4) 370c/170c day/night, well-watered, without post-anthesis fertilizer, Environment 5) 370c/170c day/night plus drought, with post-anthesis fertilizer, Environment 6) 370c/170c day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altentbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give pBluescript SK(-) phagemids in the TJ Close lab (Chin, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (others).*

152 a 2216 c 241 g 117 t

BASE COUNT

Query Match	18.7%	Score 245.6;	DB 14;	Length 726;
Best Local Similarity	66.8%;	Pred. No. 9.7e-38;		
Matches 350;	Conservative 0;	Mismatches 174;	Indels 0;	Gaps 0;
QY 682	AAGATCAACTGGCTCAAGGTGGCATATCGCCGCCACAAAGCTGGTACTGTGTGCCCC	741		
Db				
QY 200	AAGATCAACTGGATGAAGGCCGGGATCCTGAGCCCGACAAAGTGTCTCAGCGTGAGCCCC	259		
Db				
QY 742	AATACACGACCGAGATFCGTGCTGCGCATGCGCCGCCGTGTGGAGCTGGACACCGTGCATC	801		
Db				
QY 260	TACTACGCGAGGAGCTCATCTCGCGCGAAGCCAGGGGCTCGAGAGCTCGACACATCATG	319		
Db				
QY 802	CGGCCAAGGCGATTGAGGCGATTGTGAAGCGCATGACATTTGAGAGTGGAAACCCCAAG	861		
Db				
QY 320	CGCCTCACGGGCTATCACGGGCTGTCACGGCATGACGTCAGCGTAGTGGACCCCGCC	379		
Db				
QY 862	ACGACAAAGTTCCTGCTCGCGCCTACGACAGAACAGCGTCTACGCGGGCAAGCGGCC	921		
Db				
QY 380	AAGCACAAGTTCCTGCTGCTGCCAATACGAGCTGTCACCAACCGCTTGTGAGGGGGAAGGCGCTG	439		
Db				
QY 922	GCCAAGGAGGCCCTGCAAGGCGGAGCTGGGCTGCTGTGGACCCCAACCGCCCGCTGTTC	981		
Db				
QY 440	AACAAGGAGGCGCTGCAGGCGGAGGTGGGCTGCCGCTGACCGAAGGTGCCCTGGTG	499		
Db				
QY 982	GCCTTCATCGGCCCTGGAGGAGCAGAAGGTGTGGACATCATCTGGCGCGCCTGCC	1041		
Db				
QY 500	GCCTTCATCGGCAGGCTGGAGGAGCAGAAGGGCCCCGACGTGATGATCGCGCCATCCCG	559		
Db				
QY 1042	AAGATCCTGCGCCACCCCAAGGTGCAGATCGCATCTGGGTACCGCAAGGCGCCCTAC	1101		
Db				
QY 560	GAGATCTTGAAGGAGGAGCGTCCAGATCGTTCCTTGGCACCGGGAAGAGAAGTTT	619		
Db				
QY 1102	GAGAAGCTGTGTGAACGCCATCGGCACCAATACAAAGGGCGCGCAAGGGCGTGGTCAAG	1151		
Db				
QY 620	GAGCGGCTGTCTAAGACGCTGGAGGAGAAGTTCGCGAGCAAGGTGAGGGCCGTGGTCAGG	679		
Db				
QY 1162	TTCTCGCGCCCTGGCGCATGCTCAACCGCGGCGCGCACTT	1205		
Db				
QY 680	TTCAACGCGCGGTGGCTACCAAGATGATGGCGGCGCGACGT	723		
Db				

RESULT 15	AV641989	LOCUS	AV641989	532 bp	mRNA	linear	EST 15-DEC-2000
DEFINITION	AV641989	Chlamydomonas reinhardtii	5% CO2	Chlamydomonas reinhardtii	cDNA clone HCL043e06_r 5',	mRNA sequence.	
ACCESSION	AV641989						

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT	FEATURES	SOURCE
---------	----------	--------	----------	-----------	---------	-------	---------	---------	---------	----------	--------

AV641989.1 GI:10785317
EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 532)
Asamizu, E., Miura, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y., and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
20539644
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>,
Location/Qualifiers
1..532

FEATURES	SOURCE
-----------------	---------------

```

/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon.3055"
/clone="HCL043e06_1"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/notes="vector: pBluescriptII SK-; Site1: EcoRI; Site2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"

```

BASE COUNT	89 a	179 c	162 g	102 t
ORIGIN				

```
Query Match      18.6%; Score 244.2; DB 10; Length 532;
Best Local Similarity 98.8%; Pred. No. 1.7e-37;
Matches 246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY	1	CGCGTGACATCGATGTTGCTGCTGAGTGCGCCCTTGGTCCAAAGAGCGGCGCTG	60
Db	284	CGCGTGACATCGATGATGTTGCTGCTGAGTGCGCCCTTGGTCCAAAGAGCGGCGCTG	343
QY	61	GGCGATGTGACTGGTGGCCCTGCTATTGAGTGTGAAGCGCGCCACCGCGTCATGACC	120
Db	344	GGCGATGTGACTGGTGGCCCTGCTATTGAGTGTGAAGCGCGCCACCGCGTCATGACC	403
QY	121	ATTGCCCTCGCTACGACCAGTAGCTGAGCGCTGGGACACCTCGTGGTGGTGGACATC	180
Db	404	ATTGCCCTCGCTACGACCAGTAGCTGAGCGCTGGGACACCTCGTGGTGGTGGACATC	463
QY	181	ATGGCGGAGAGGTCCGCTACTTCCACTCCATCAAGAGGGCGTGCACCCGGTGTGGATT	240
Db	464	ATGGCGGAGAGGTCCGCTACTTCCACTCCATCAAGAGGGCGTGCACCCGGTGTGGATT	523
QY	241	GACCACCC	249
Db	524	GACCACCC	532

Search completed: June 3, 2003, 15:27:27
Job time : 1288.02 secs

This Page Blank (uspto)

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 09:49:44 ; Search time 31.6082 Seconds
(without alignments)
12748.991 Million cell updates/sec

Title: US-09-980-771A-6

Perfect score: 1314

Sequence: 1 gcctgacacgtgattggt.....gcggccctggtgcacacgtc 1314

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCUTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	400.6	30.5	2267	4	US-08-679-645-25
2	388.4	29.6	2542	3	US-08-941-445A-6
3	237.2	18.1	2067	4	US-09-388-743-21
4	236.8	18.0	2274	4	US-09-388-743-17
5	218.8	16.7	2176	4	US-09-388-743-13
6	216.8	16.5	2202	4	US-09-388-743-1
7	202.6	15.4	2825	4	US-09-196-390-5
8	199.6	15.2	2380	1	US-08-572-951-3
9	193.2	14.7	2097	3	US-08-941-445A-10
10	191.4	14.6	2248	4	US-09-345-214-20
11	191	14.5	1798	4	US-09-345-214-16
12	191	14.5	2019	4	US-09-345-214-15
13	151.2	11.5	2007	3	US-08-941-445A-8
14	151.2	11.5	2085	1	US-08-572-951-2
15	116.8	8.9	2239	4	US-09-196-390-1
16	109	8.3	2348	4	US-09-388-743-5
17	106.4	8.1	2418	4	US-09-388-743-25
18	103.6	7.9	1758	3	US-08-836-567-3
19	102.2	7.8	2360	3	US-08-836-567-9
20	101.4	7.7	1528	4	US-09-345-214-6
21	101.4	7.7	1620	3	US-08-941-445A-20
22	101.4	7.7	1752	3	US-08-941-445A-12
23	101.4	7.7	2008	4	US-09-345-214-12
24	101.4	7.7	2491	4	US-09-345-214-5
25	99.8	7.6	2383	4	US-09-192-909-1
26	97.4	7.4	4800	3	US-08-941-445A-4
27	96.6	7.4	2990	1	US-08-572-951-1

28	88.4	6.7	2793	3	US-08-836-567-7	Sequence 7, Appli
29	86.4	6.6	6027	2	US-08-968-542C-1	Sequence 1, Appli
30	83.6	6.4	1926	3	US-08-836-567-5	Sequence 5, Appli
31	82.6	6.3	1464	1	US-07-735-065-1	Sequence 1, Appli
32	82.6	6.3	1464	1	US-08-469-202-11	Sequence 11, Appli
33	82.6	6.3	1464	2	US-08-484-434C-11	Sequence 11, Appli
34	80.6	6.1	2277	1	US-08-676-967-5	Sequence 5, Appli
35	80.6	6.1	2277	2	US-09-098-487-5	Sequence 5, Appli
36	80.6	6.1	2277	2	US-09-098-487-5	Sequence 5, Appli
37	78.4	6.0	2549	1	US-08-470-720-2	Sequence 2, Appli
38	78.4	6.0	4964	1	US-08-470-720-2	Sequence 2, Appli
39	68.2	5.2	1601	3	US-08-735-491-1	Sequence 5, Appli
40	66.2	5.0	2303	3	US-08-836-567-1	Sequence 1, Appli
41	66.2	5.0	4168	3	US-08-836-567-11	Sequence 11, Appli
42	65.2	5.0	1722	4	US-09-385-028-15	Sequence 15, Appli
43	65.2	5.0	11604	4	US-09-385-028-13	Sequence 13, Appli
44	65.2	5.0	15079	4	US-09-385-028-1	Sequence 1, Appli
45	64.4	4.9	44377	2	US-08-804-227C-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-679-645-25
; Sequence 25, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 25:

Db	1267	AGTACATCGCGGTGAAGTAGTACGAGCTGTCCAGCGCGCTGGAGGCGCTGAACAAGG	1326
Qy	929	AGGCCCTTCAGAGCCGAGCTGGCGCTGCCTGTGTGGACCCACCGCGCCCTGTTCGCCCTTCA	988
Db	1327	AGCGCTGCAGCGGAGGTTCGGGCTCCCGGTGGACCGGAAACATCCCGCTGGTGGCGTTCA	1386
Qy	989	TCGGCGCCTGGAGGAGCAAGAGGTGTGGACATCATCTTGGCGCGCCCTGCCCAAGATCC	1048
Db	1387	TCGGCAGGCTTGAAGAGCAGAAGAGAACCGAGCTCATGGCGCGCGCCATCCCGCAGCTCA	1446
Qy	1049	TGGCCACCCCCAAG---GTGCAGATTCGCATCCTTGGTACCGGCAAGCGCGCCTTACGAGA	1105
Db	1447	TGGAGATGGTGGAGGAGCTGCAGATCGTTCTCTCTGGCGACCGGCAAGAAGATTCGAGC	1506
Qy	1106	AGCTGGTGAACGCATTCGGCACCACCAAGTACAAGGGCGCGCCCAAGGGCGTGGTCAAGTTCT	1165
Db	1507	GCATGCTCATGAGCGCGGAGGAGAGTTCCACGGAAGCTGGCGCGCTGGTCAAGTTCA	1566
Qy	1166	CGCGCGCCCTGGCGCACATGCTCACCGCGCGCGCCGCTCATGCTGGTGCCTTCGCGCT	1225
Db	1567	ACGGCGGCTTGGCGCACCATCATGGCGCGCGCGCGAGTGTGTCGCCGTCAACAGCGCT	1626
Qy	1226	TCGAGCCTTGGCGCTGATCCAGCTTCGAGCGCCATGCATCTAGGTACCGTGCCTGGTGTAG	1285
Db	1627	TCGAGCCTTGGCGCTCATCCAGCTTCGAGGAGTGCATCGGAACGCCCTTGGCGCTGGC	1686
Qy	1286	CTCTCACCGCGCGCTTGGTCGACACCGTC	1314
Db	1687	CGTCCACCGTGGACTCGTCGACCAATC	1715
RESULT 2			
US-08-941-445A-6			
; Sequence 6, Application US/08941445A			
; Patent No. 6107060			
; GENERAL INFORMATION:			
; APPLICANT: Keeling, Peter			
; APPLICANT: Guan, Hanping			
; TITLE OF INVENTION: Starch Encapsulation			
; NUMBER OF SEQUENCES: 37			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.			
; STREET: 5370 Manhattan Circle			
; CITY: Boulder			
; STATE: CO			
; COUNTRY: US			
; ZIP: 80303			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/941,445A			
; FILING DATE: 30-SEP-1997			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 60/026,855			
; FILING DATE: 30-SEP-1996			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Winner, Ellen P			
; REGISTRATION NUMBER: 28,547			
; REFERENCE/DOCKET NUMBER: 89-97			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (303) 499-8080			
; TELEFAX: (303) 499-8089			
; INFORMATION FOR SEQ ID NO: 6:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 2542 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: not relevant			
; MOLECULE TYPE: cDNA to mRNA			

```
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 453..2282
US-08-941-445A-6

Query Match      29.6%; Score 388.4; DB 3; Length 2542;
Best Local Similarity 59.1%; Pred. No. 2e-67;
Matches 795; Conservative 0; Mismatches 461; Indels 90; Gaps 4;

QY 5 TGGACATCGTAGTGGCTGCTAGCTGCGCCCTTGGTCAAGAGGGGGGGCTGGCG 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 TGAACGTCGTGTTGCTGGCGCCGAGATGGCCCTGGAGCAAGACCGCGCTCGGTG 759
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 65 ATGTGACTGTGTGGCTGCTATTTAGCTGTGTCAGCGCGGCCCATGATGACCATG 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 ACPCTCTGTGGCTCCCTCCCTGCCATGGCTGCGATGGCCAGAGGTGATGTGATCT 819
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 125 CCCCTCGCTAGGACCTAGCTGACGCTGGGGACACCTGGTGGTCTGTGGACATCATGG 184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 CTCCTCGTACGACCTAGCAAGACACCTGGGATACAGCGTTGTGGCTGAGATCAAGG 879
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 185 -----GGAGAAGTCCGCTACTTCCACTCCATCAAGAAAGGGGTGCAACGG 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 TTGCAGACAGTACGAGAGGTGAGGTTTTCATGCTCAACGCTGGAGTGCACCGTG 939
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 233 TGTGGATTGACCCCTCGTTCCTGGCCAAAGTCTTGGGGCAAGACCGGCTTCCAAAGCTGT 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 940 TGTTCATCGACCATCCGCTCATCTCTGAGAAAGTTTGGGNAAGACCGGTGAGATCT 999
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 293 ACGGCCCTCGCTCGGCGCTGACTACTGACACCAACAGCGCTTCGCCCTGTCTGCA 352
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1000 ACGACCTGACATGGAGTTGATTAAGAAAGACACCAAGATGCTTTCAGCCTTCTTGCC 1059
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 353 AGCGCGCTATTGAGCTGCGCGGTGCTGCCCTTCGCGCCGCTC----- 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1060 AGCAGCACTCGAGGCTCTAGGATCTTAACCTCAACAAACACCCATACTTCAAGAA 1119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 394 -----GGCAGGAGTGTGCTGTGGCCCAACGACTGGCACTCGCGCTGTGCGCGTCC 448
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1120 CTTATGTGTGAGGATGTGTGTTGCTGTGCAACGACTGGCACTGGCCCACTGGCGAGCT 1179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 449 TGTGTAGGAGGAGTACCAACCCCAAGGGCGATTCACCAAGGCCAAGTGGTGTGCTA 508
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1180 ACCTGAAGAACAACCTACAGCCCAATGGCATCTACAGGAATGCAAGGTTGCTTCTGCA 1239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 509 TCCACAACATCGCTTCCAGGGCGGCATGTGGGAGGAGGCTTTCAAGGACACAGAGTGC 568
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1240 TCCACAACATCTCTTACAGGGCGGTTCGCTTTCGAGGATTAACCTGAGCTGAACCTCT 1299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 569 CCAAGGCGGCTTTGACAAGCTGCGCTTCTCGACGCGCTATGCCAAGGTTTACACTGAGG 628
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1300 CCGAGAGGTTTCAGTCTATCTCGATTTTCATCGACGGGTATGAC----- 1343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 629 CCACCCCATGAGGAGGACAGAGCCCGCTGACGGGAAGACCTCAAGAAATCA 688
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1344 -----ACGCGGGTGGAGGGCAGGAAGATCA 1368
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 689 ACTGGCTGAAGGTTGGCATTATGCGCGCGACAGCTGGTGAATGCTGCCCAACTACG 748
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1369 ACTGGATGAAGCGCGAATCTGGAAGCCGACAGGAGGTGCTACCGTGAAGCCCGTACTACG 1428
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 749 CGACCGAGATCGTTCGGATCGCGCGCTGTGTGGAGCTGGACACCGCTCATCGCGCCA 808
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1429 CCGAGGAGCTCATCTCGGCATCGCCAGGAGTGCAGACTCGCAACATCATGCGGCTCA 1488
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 809 AGGCATTGAGGATGTGTGAAGCGCATGGACATTTAGAGTGAAGCCCAAGACCGACA 868
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1489 CCGGCATCACCGGCATGCTCAAGGGCATGGACGTCAGCGAGTGGATCTCTAGCAAGACA 1548
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 869 AGTTCCTGTGCGCCCTACGACCAAGACAGCTCTACGCGGCAAGCGCGCCCAAGG 928
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
Db 1549 AGTACATCACGCCCAAGTACGACGCAACAGCGCAATCGAGCGAAGCGCTGAACAAGG 1608
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 929 AGGCCCTGAGCGCGAGCTGGCGCTGCTGTGGACCCACACCGCCCTGTTCGCGCTTCA 988
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1609 AGCGCTTGCAGCGGAGCGGGGTCTTCGGTGCAGAGAAATCCCACTGATCGCGTTCA 1668
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 989 TCGCCGCTGTGAGGAGCAGAAAGGTGTGGACATCATCTGCGCCCTGCCCCAAGATCC 1048
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1669 TCGCAGSCTGAGGAACAGAAAGGCCCTGACGTCATGCGCGCCCATCCCGAGCTCA 1728
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1049 TGGCCACCCCAAGGTGCAGATCGCCATCTCTGGGTACCGGCAAGCCCGCTACGAGAAGC 1108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1729 TG---CAGGAGGAGCTCCAGATGCTTCTGCTGCTACTGGAAGAAAGATTCGAGAAGC 1785
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1109 TGTGAACGCCATCGGCACCAAGTACAAGCGCGCGCAAGCGGTGCTCAAGTTCTCGG 1168
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1786 TGCTCAAGAGCATGGAGGAGAGTATCCGGCAAGGTGAGGCGGTGTTGAAGTTCAACG 1845
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1169 CGCCCTTGGCCACATGCTACCGCGCGCGCGACTTTCATGCTGTGCGCTCGCGCTTCG 1228
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1846 CGCGCTTGTCTATCTCATCATGCGCGAGCGAGCTGCTCGCGTCCCGAGCGCTTCG 1905
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1229 AGCCTGCGGCGCTGATCCAGCTGCACGCCATGCACCTACGTAACGTCGCGCTGGTAGCCT 1288
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1906 AGCCTTGTGACTCATCCAGCTGCAGGGATGAGATACGGAACGCCCTGTGCTTGGCGGT 1965
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1289 CCACCGCGCGCTGTGTCACACACCGTC 1314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1966 CCACCGGTGGCTGTGGACACGGTC 1991
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 3

US-09-388-743-21

; Sequence 21, Application US/09388743

; Patent No. 6423886

; GENERAL INFORMATION:

; APPLICANT: Singletary, George

; APPLICANT: Zhou, Ian

; TITLE OF INVENTION: No. 6423886el Starch Synthesis Polynucleotides and Their

; TITLE OF INVENTION: Use in the Production of New Starches

; FILE REFERENCE: 1144

; CURRENT APPLICATION NUMBER: US/09/388,743

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 21

; LENGTH: 2067

; TYPE: DNA

; ORGANISM: Tulipa fosteriana

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (58)...(1857)

US-09-388-743-21

Query Match

Best Local Similarity 18.1%; Score 237.2; DB 4; Length 2067;

Matches 702; Conservative 0; Mismatches 558; Indels 90; Gaps 4;

```
QY 1 GCGCTGACATCGTAGTGGTGTGCTGAGTGTGCGCCCTTGGTCCAAAGACGCGCGGCTG 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 GGGATGAACCTGTGTTTCGTGGGACGAGACGGGTCCGTACAGAAAGACGCGCGGCTC 330
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GCGCATGTGACTGTGGCTGCGCTTATGAGTGTCAAGCGCGCCACCGCTCATGACC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 GGGATGTGTAGGAGGTACCCCGCTTGGCGGAGAGGAGCATCGGTCTATGGTT 390
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 ATTGCCCTCGTACGACCACTACGCTGACGCTTGGGACCTCGTGGTGTGGACATC 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 391 GTCACCTCCGGGTACGATCATCAAGATGATCAAGAGTGCATGGGACACAAACTGCTTGTGATGC 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 ATGGGC-----GAGAAGTCCGTACTTCCACTCCATCAAGAGGCGGTGCAC 228
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


Db 1258 AAGCTTTTCAAGCTGAGTGTGGGCTGCTGTTTAAACAAAAAAGCTGTTTGGGCTTGG 1317
QY 989 TCGCCGCGCTGAGAGCAGAGAGGTGTGGACATCATCTGCGCGCCCTGCCCAAGATCC 1048
Db 1318 TTGGAAGACTAGATGAGCAGAAAGGCTCAGACATCTTAGCTGCAGCAATTCAGAACTTC 1377
QY 1049 TGGCCACCCCAAGCTGCGAGATCGCCATCTCGGTACCGGCAAGCGCGCTACGAGAAGC 1108
Db 1378 TTGTGAG---AATGTTCAAGTATAGTACTTGGCAGCTGGCAGAGAGAGTTGGAGAGTG 1434
QY 1109 TGGTGAAGCCCATPCGGACCAAGTACAGAGGCGCGCGCCGCAAGGGGTGGTCAAGTCTTCGG 1168
Db 1435 AACTTACATTAATTGAGGAATGTTTCCAGACAAATTCAGACACATCTCAAAATTCAGAG 1494
QY 1169 CGCCCTGCGCAGCATGCTCACCGCGCGCGGAGCTTCAATGCTGGTGGCCCTCGCGCTTCG 1228
Db 1495 TTCCCTTAGCTCATGCAATCATGGCAGGAGCTGATATCTTGTATTCAGCAGATTCG 1554
QY 1229 AGCCCTGCGGCTGATCCAGCTGCAGCCCATGACACTACGGTACCGGTGGTAGCCT 1288
Db 1555 AACCCCTGTGGCTCATTCAGCTTACGGCCATCGATATGGAATCTCCCTATGTGTAGCA 1614
QY 1289 CCACCGCGCGCTGGTGCACACGTC 1314
Db 1615 CCACCTGGTGGACTTGTGACACTGTC 1640

RESULT 6
US-09-388-743-1
; Sequence 1, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Zhou, Lan
; APPLICANT: Singletary, George
; TITLE OF INVENTION: No. 6423886el Starch Synthese Polynucleotides and Their
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2202
; TYPE: DNA
; ORGANISM: Curcuma zedoaria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (130)...(1974)
US-09-388-743-1

Query Match 16.5%; Score 216.8; DB 4; Length 2202;
Best Local Similarity 51.6%; Pred. No. 5e-34;
Matches 694; Conservative 0; Mismatches 562; Indels 90; Gaps 5;

QY 5 TGGACATCGTGTGTTGCTGTGAGTGTGCGCCCTTGGTCCAGAGCGGGCGCTGGGG 64
Db 395 TGAACCTGATCTTGTGTGCTGAGTGTGCTGCGTGGAGTAAACTTGGAGGGCTTGGT 454
QY 65 ATGTGACTGTGSCCTGCTTATGACTGTCTAAGCGCGGCCACCGCTCATGACCATG 124
Db 455 ATGTGCTTGGAGTTTGGCCACCGGCTATGGCGCAAGGAGACACAGGGTGTGACTATAG 514
QY 125 CCCTCGCTACGACAGTACGCTGAGCGCTGGGACACCTCGGTGGTGGGACATATG 184
Db 515 CACCGGACATGACCAATCAAGATGATGGATACGCTGTCTTGTGAGTTGAAAG 574
QY 185 -----GCGAGAGGTCGCTACTTCCACTCCATCAAGAGGCGTGCACCGG 232
Db 575 TTGGTGATAGAAATTTGAGTGTGCTGCTTTCCTGCTGCTACAAAAGGGAGTTGATCGG 634
QY 233 TGTGGATTGACCAACCCCTGTTCTGCGCAAGTCTGTGGCGAGACCGCTCCAACTGT 292
Db 635 TGTGTGGATCAACCTCTCTTCTTGTGAGAAGGTTTGGGGAAGAACTGGAGGAAGATAT 694

QY 293 ACGGCCCGCTCCCGCGCTGACTACCTGGACAACACAGCGCTTCGCGCTTCTTGA 352
Db 695 ATGGCTCTGTACAGAACTGATTATGAAGACAACAGCTAAGGTTCTGTCTTCTGT 754
QY 353 AGGCCCTATTTAGGCTGCCCGCGTGTG-----CCCTTCGGCC 391
Db 755 TGGCAACTCTGGAACCTCCAAAGGTTCTGAATCCCLACAAATAACAAATATCATCTGGAC 814
QY 392 CCGGCAGAGACTCGCTTCTGTTGGCAAGCACTGGCACTCCGCGCTGGTGGCGCTCTGC 451
Db 815 CAAAAGTGAAGATTTATTTATTTGCTAAGCTTGGCTATCTGCTCTATACCTTGTAT 874
QY 452 TGAAGAC---GAGTACCAGCCCAAGGGCCAGTTCCACCAAGCAAGTCCGCTGGCTA 508
Db 875 TAAAGACCATTTATATCAAGCCCATGGAATATACAAAATGCTAAAGTTGCTTCTGCA 934
QY 509 TCCACAACATCGCTTCCAGGCGCGCATGTGGAGAGGCTTTCAAGGACACCAAGCTGC 568
Db 935 TTCTAATATTTGCTATCAGGGACGTTTGCCTTTTGAAGATTTTTCGCGTCTCAATCTCC 994
QY 569 CCACGCGCGCTTTGACAAGCTGCGCTCTCGGACGCTATGCCAAGTTTACACTGAGG 628
Db 995 CTGATACATTCAGTCTCTTTTGTATTTTCATGATGCTATGCAAA----- 1040
QY 629 CCACCCCATGGAGGAGCAGAGACCCCGCTGAGGGGAAGACCTACAGAAGATCA 688
Db 1041 -----ACCATAAAGGAAGGAAATCA 1063
QY 689 ACTGGCTGAAGGTGGCATATATCGCCGCCACAAAGTGTGTGACTGTTCGCCCACTACG 748
Db 1064 ACTGGATGAAGCGGGAATATAGAAATCAGATCGTGCATGACTGTGAGGCCATCTATG 1123
QY 749 CGACCGAGATCGTGCAGTGTCCGCGGTGTGGAGCTGGACACCGTCTATCGCGCCA 808
Db 1124 CCAGAACTCTCTCAGGATCGATAAGGCGTCCAGTTGGACATATATCTGGCTGA 1183
QY 809 AGGCAATTGAGGCATTTGACCGCATGTGACATTTAGGAGTGGAACTCCCAAGACGACA 868
Db 1184 AAACCATCTGTGGCATCATAAATGGAATGGACACCAAGAGTGAATCCCTCAACAGACA 1243
QY 869 AGTTCCTGTCTGCGCCCTACGACCAAGAGCTCTACCGCGCAGGCGCGCCCAAGG 928
Db 1244 AATACATAACAGCAAAATACGACGCAACCACTGTATGGAGGCAAGCCACTCAACAGG 1303
QY 929 AGGCCCTGACGCGGAGCTGGGCTGTGCTGTGACCCGCCACCGCCCTGTGCGCTTCA 988
Db 1304 AAGCTTTGCAAGCTGAGTTGGACTGCCCGTCAACAGTAAATCCCTGTGATAGCTTCA 1363
QY 989 TCGCGCGCTGGAGGAGCAGAGGTGTGACATCATCTGCGCGCGCTGCGCGCTGCCAAGATCC 1048
Db 1364 TTGGCAGACTAGAAGAACAAAGGTTTACAGCATTTCTAGCTGAAGCAATTCCAAAGTCT 1423
QY 1049 TGGCCACCCCAAGGTGCAGATCGCCATCTCGGTACCGGCGCAAGGCGCTGCTCAAGTTC 1108
Db 1424 T---CGATCAGAGATTTCAAGTGTATGTTCTCGGTACTGTGTAAGAAAGATGAGCGCC 1480
QY 1109 TGGTGAAGCGCATCGGCACCAAGTACAAAGGCGCGCAAGGCGCTGCTCAAGTTCFCGG 1168
Db 1481 AACTTGCATTTGCTGAGGACGAGTTCACAGCAAAATTCAGAGCTCATATGAAGTTCAATA 1540
QY 1169 CGCCCTTGGCGCATGCTCACCGCGCGCGCACTTCATGCTGGTGGTCCCTTCGGGTTCG 1228
Db 1541 TTCCCTTGGCTCATGGAATCATGCGGGTGTGTATATCTTGTATTCAGGAGTGTG 1600
QY 1229 AGCCCTGCGGCTTATCCAGCTGCACGCCATGCACTACGCTACGCTGCGCTGTCGCT 1288
Db 1601 AACCTGCGCTCATTTCACTGCTCAGGGCATGAGATACGGAACCCCTTCTCATGTGACCA 1660
QY 1289 CCACCGCGCGCTGGTGCACACCGTC 1314
Db 1661 CGACTGTGGCTCGTGCACACTGTC 1686

1631 ARGNGTNGAYATHATGCGNGAYCNCNATHCAITGGATH--GCNGNCARGAYTNCARY 1687
QY 1070 TCGCCATCTCGGTACCGGCAAGCCGCCACGAGAGCTGGTGAAGCCATCGGCACCA 1129
Db 1688 TNGTNGTNGGNGNCGNGAYTNGARGAYATGYTNMGNMNTTYGARWSNG 1747
QY 1130 ASTACAGGCGCGCCGCAAGGCGTGTCAAGTCTCGGCGGCCCTCGGCGACATGCTCA 1189
Db 1748 ARCAWSNGAYARGTNMGNGCNTGGGTNGGNTTWSNGTNCNNTYNGCNCAYMGNATHA 1807
QY 1190 CCGCCGCGCGGACTTCATCTGCTGCGCTCGGCTTCGAGCCCTCGGCTGATCCAGC 1249
Db 1808 CNGCNGGNGCNGAYATHYNTNATGCCNWSNMNTTYGARCCNTGYGNTYTRAYCARY 1867
QY 1250 TGCACGCCATGCACTAGCGTACCGTCCGCTGGTGGTCCGCTCCACCGCGGCGCTGCTGACA 1309
Db 1868 TNYAGCNATGGCNTAYGNGACNGTNCNGTNGTNCAYGCGNGTNGGNGNTYNGMNGAYA 1927
QY 1310 CCGT 1313
Db 1928 CNGT 1931

RESULT 9

US-08-941-445A-10
; Sequence 10, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2097 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2097
US-08-941-445A-10

Query Match 14.7%; Score 193.2; DB 3; Length 2097;
Best Local Similarity 51.8%; Pred. No. 2e-29;
Matches 694; Conservative 0; Mismatches 538; Indels 108; Gaps 7;
QY 1 GCGCTGACATCGTGTGCTGCTGAGTCCGCCCTTGGTCCCAAGACGGGGCGCTG 60
Db 616 GTGATGAACGTCGCTGGTGGCTTCTGAATGTCTCTTCTTCAAGACAGGTGGCCTT 675
QY 61 GCGCATGTGCTGCTGCTGCTTATTCAGTCTGCTCAAGCGCGCCACCGCTGATGACC 120
Db 676 GGAGATGTGCTGGTGGCTTGGCTTAAGCTCTGCGAGAGAGACACCGTGTATGTC 735
QY 121 ATTGCCCTCGCTACGACAGTACGCTGACGCTGGGACACCTCGGTGGTGGACATC 180
Db 736 GTGATACCAAGATATGAGAGATATGCCGAGCCCGGG--ATTAGGTGTAGAGAGAGCTT 793
QY 181 ATGGCCGAGAGGTCCGCTACTTCCACTCCATCAAGAGGCGGTGACCGCGTGTGAT 240
Db 794 ACAAGGTAGCTGGACAGGATTCAAGATTACTTATTTTCACTTTACATTTGATGAGTTG 853
QY 241 GACCACCCCTGGTTCCTGGCCCAAGTCTGGGGCAAGACCGGCTCCAAGCTTACGGCCCC 300
Db 854 ATTTGTATTCTGTAAGACCCCTCCCTTCGGGCAC-----CGGCACAATAAT 900
QY 301 CGTCCGCGCTGACTACCTGGACACCAACAGCGCTTCGCCCTGTCTGCAAGCGCGCT 360
Db 901 ATTTATGGGGAGAAAGATTGATATTTGAAGGCCAIGATTTTGTCTTCAAGCGCGCT 960
QY 361 ATTGAGCTGCCGCGTGTGCTGCCCTTCGGC-----CCGCGGAGGACTGCGTC 408
Db 961 GTTAGGTTCCTGATGCTTCCATGTGGGTGCTGCTATGCTGATGCTGCAACTTAGTT 1020
QY 409 TCGTGCCCAACGACTGCGCTCGCCCTGCTGCCCTGCTGCTGAGAGGAGGACTACAG 468
Db 1021 TTTCTGCTAATGATGGCATACCGCACTTCTGCTGCTCTATCTTAAAGGCTTATTCGG 1080
QY 469 CCCAAGGGCCAGTTCACCAAGGCGCAAGTGGTGTGCTATCCACACATCGCTTCCAG 528
Db 1081 GACAAATGTTGATGCAAGTATGCTGCTGCTGCTGTGATACACACATTTGCTCATCAG 1140
QY 529 GCGCGCATGTGGGAGGAGGCTTTCAAGGACACGAAGTGCCTCCAGCGCGCTTGTGACAAG 588
Db 1141 GGTGCGTGGCCCTGTAGACGACTTGGTCAATTTTGACTTGGCTGAACACTACATCGACAC 1200
QY 589 CTGGCTTCTCGGAAGGCTATGCCAAGTTTACACTGAGCCACCCCGCATGAGGAGGAC 648
Db 1201 TTCAAACTGTATGACACATTTGGTGGGATCACAG----- 1235
QY 649 GAGAAGCCCCGCTGACGGGAAAGACCTACAAGAAGATCAACTGGCTGAAGGGTGCATT 708
Db 1236 -----CAACGTTTTTGTGCGGGGCTG 1257
QY 709 ATGCGCGCGCACAAAGCTGGTGAAGTCTGCCCAACTACGCGACCGAGATCGCTGCGGAT 768
Db 1258 AAGCGCGACACCGGGTGGTGAACCTTAGCAATGGTGTACATGTGCGAGCTGAAGACTTCG 1317
QY 769 GCGCGCGGGGTGTGGAGCTGGACCGCTCATCC---GCGCCAAAGGCGCATTTAGGGCAT 825
Db 1318 GAAGCGGGTGGGCGCTCCAGCATCATAAACCAAGACACTGGAAGCTTGAAGGCGATC 1377
QY 826 GTGAACGGCATGGCAATGAGGAGTGAACCCCAAGACCGACAAAGTTCCTGTCTGCGGCC 885
Db 1378 GTGAACGGCATCGACATGAGCGAGTGAACCCCGCTGTGAGCTGCACTCCACTCCGAC 1437
QY 886 TAGGACCAACAGC-----GTCTAGCGCGCAAGGCGCCCGCCCAAGAGGCGC 933
Db 1438 GACTACCAACTACAGCTTCGAGACGCTGGACCGGCAAGCGGAGTGAAGGCGCGC 1497
QY 934 CTGAGGCGGAGCTGGGCTGCTGTGGACCCCGCCCGCCCTGCTGCGCTTCATCGCG 993
Db 1498 CTGAGGCGGAGCTGGGCTGCGAGGTTCGCGCGAGGCTGCACATGATCGGTTTCATCGG 1557

QY 699 GGGTGGCAATTATCGCCGCGGACAAAGCTGGTGAAGTGTGCGCCCAACTAGCGACCGAGAT 758
Db 1170 GTGTGTTCTGAAGATGGCAGACCGGCTGTGACATCTCAGCCGCGCTACCTGTGGAGCT 1229
QY 759 CGCTCGGATGCGCCGCGGCTGGAGCTGGAGCTGACACCGTGC---ATCCGGGCGCAAGGGCAT 815
Db 1230 CAAGACAGTGGAAAGCGGCTGGGGCTCCACACATCATCCCTTCTAAGAGCTGGAAAT 1289
QY 816 TGAGGCGATGAGACGCAATGAGCATTCAGAGTGGAGTGGACCCCAAGACGACCAAGTCTCT 875
Db 1290 CAATGCAATCTGAACGATCGACATCGACACAGAGTGGACCCCAAGTGGAGCTGCACCT 1349
QY 876 GTCTCGGCGCTACGACCAAGACAGG---TCTACGCGCGCAAGCGCGCGC 923
Db 1350 GCGGTGCGAGGCTACACCAACTACTCTCTCGAGACACTCGACGCTGGAAAGCGGCAAGT 1409
QY 924 CAAGAGCGCTGCGAGCGGCTGGGCTGCTGTGAGACCCACCGCCCGCTGTTCG 983
Db 1410 CAAGCGCGCGCTGCAAGCGGAGCTGGGCTGGAAGTGGCGGAGACGCTGCCGCTGCTCGG 1469
QY 984 CTTATCGGCGCGCTGGAGGAGCAAGAGTGTGACATCATCTCGCGCGCGCTGCCCAA 1043
Db 1470 CTTATCGGCGCTGGAGTGGAGGAGCAAGAGTGTGACATCATCTCGCGCGCGCTGCCCAA 1043
QY 1044 GATCTGGCGCCACCCCAAGTGCAGATCGCCATCTGCTGGTACCGGCAAGCGCGCTTACGA 1103
Db 1530 GATCGCG---GGCAGGAGCTGAGCTGTGATCTGGGACCGCGCGCGCTGACCTGGA 1586
QY 1104 GAAGCTGTGAAGCGCATCGGACCAAGTACAAAGGCGCGCGCGCTGCTCAAGTT 1163
Db 1587 ACGAATGCTGCAAGCACTTGGAGCGGAGATCCCAAGAGTGGCGGCTGGTGGT 1646
QY 1164 CTCGGCGCGCTGGGCGCAATCTACCGCGCGCGCGCTTCTATCTGCTGGTGGCTCGCG 1223
Db 1647 CTCGGTCTAATGTTGATCGATCGATCAGCGCGCGCGCGCTGCTGCTGATGCTCGCG 1706
QY 1224 CTTGAGCGCTGCGCGCTGATCGAGTGCAGCGCATGCTAGCTAGCTGCTGCTGCTGCTGCT 1283
Db 1707 CTTG---CCGGCGGCTGAACGAGCTTACGCGATGGCATAGGCGCGCTGCTGCTGCT 1763
QY 1284 AGCTTCCACCGCGCGCTGCTGACACCGT 1313
Db 1764 GCAGCGCTGGCGGCGCTCAGGACACCGT 1793

RESULT 14

US-08-572-951-2
; Sequence 2, Application US/08572951
; Patent No. 5824790
; GENERAL INFORMATION:
; APPLICANT: KEELING, PETER L.
; APPLICANT: KNIGHT, MARY E.
; APPLICANT: GUAN, HANPING
; TITLE OF INVENTION: MODIFICATION OF STARCH
; TITLE OF INVENTION: SYNTHESIS IN PLANTS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: Pillsbury Madison & Sutro LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,951
; FILING DATE: 15-DEC-1995

; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,602
; FILING DATE: 29-NOV-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/263,921
; FILING DATE: 21-JUN-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul N. Kokulis
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 222957/1.02.15C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-572-951-2
Query Match 11.5%; Score 151.2; DB 1; Length 2085;
Best Local Similarity 57.3%; Pred. No. 3e-21;
Matches 361; Conservative 0; Mismatches 248; Indels 21; Gaps 4;
QY 699 GGGTGGCAATTATCGCCGCGGACAAAGCTGGTGAAGTGTGCGCCCAACTAGCGACCGAGAT 758
Db 985 GTGTGTTCTGAAGATGGCAGACCGGCTGTGACATCTCAGCCGCGCTACCTGTGGAGCT 1044
QY 759 CGCTCGGATGCGCCGCGGCTGGAGCTGGAGCTGACACCGT---ATCCGGCGCAAGGGCAT 815
Db 1045 GAAGACAGTGGAGCGGCTGGGCGCTCCACAGACATCATCCGTTCTAACGACTGGAAGT 1104
QY 816 TGAGGCGATGTAAGCGCATGAGCATTTAGGAGTGGACCCCAAGACCGCAAGTTCCT 875
Db 1105 CAATGCAATCTGAAGCGCATCGGACCAAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1164
QY 876 GTCTGCGCGCTACGACCAAGACAGCG---TCTACGCGCGCAAGCGCGCGC 923
Db 1165 GCGTGGAGCGGTACACCAACTACTCTCTCGAGACACTCGACGCTGGAAGCGCGAGTG 1224
QY 924 CAAGAGCGCGCTGCGAGCGCGAGCTGGGCGCTGCTGTGAGACCCCAAGCGCGCGCTGTTCG 983
Db 1225 CAAGCGCGCGCTGCGAGCGGAGCTGGGCGCTGGAAGTGGCGGAGACGCTGCGCTGCTCGG 1284
QY 984 CTTATCGGCGCGCTGGAGGAGCAGAGGCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1043
Db 1285 CTTATCGGCGCGCTGGATGGACAGAGGCGGTGGACATCATCGGGAGCGGATGCGCGTG 1344
QY 1044 GATCTGGCGCACCCCAAGGTGCGCATCTCTGGGTACCGGCAAGCGCGCTTACGA 1103
Db 1345 GATCGCG---GGCAGGAGCTGAGCTGTGATCTGGCGCGCGCGCTGACCTGGA 1401
QY 1104 GAAGCTGTGAAGCGCATCGGACCAAGTACAGGGCGCGCGCAAGGGCGTGGTCAAGTT 1163
Db 1402 ACGAATGCTGAGCACTTGGAGCGGAGCATCCCAAGAGTGGCGGCTGGGTT 1461
QY 1164 CTGCGCGCGCTGGCGCACATGCTCACCGCGCGCGCTTCTATCTGTGCTGCTCGCG 1223
Db 1462 CTCGGTCTAATGTTGATCGCATCAGCGCGGCGCGCGGCTGCTGTGTGTGATGCTCGCG 1521
QY 1224 CTTGAGCGCGCTGGGCGCTGATCCAGTGCAGCGGCTGCACTGCACTGCACTGCACTGCACTGCT 1283
Db 1522 CTTG---CCGGCGGCTGAGCAGCTTACGCGATGGCATACGGCACCGCTCCTGTGTT 1578
QY 1284 AGCTTCCACCGCGCGCTGCTGACACCGT 1313
Db 1579 GCAGCGCTGGCGGCGCTCAGGACACCGT 1608

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: June 6, 2003, 21:49:59 ; Search time 119.284 Seconds
(without alignments)
15416.986 Million cell updates/sec

Title: US-09-980-771A-6

Perfect score: 1314

Sequence: 1 gcgcggacatcgatggt.....gcggcctggtgcacaccatc 1314

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400.6	30.5	2267	9	US-09-961-077-25
2	245.6	18.7	2399	9	US-10-138-075-1
3	237.2	18.1	2179	9	US-10-138-075-3
4	202.6	15.4	2825	10	US-09-952-677-5
5	116.8	8.9	2239	10	US-09-952-677-1
6	94.2	7.2	790	10	US-09-966-881-44
7	82.8	6.3	1427	10	US-09-974-300-757
8	82.2	6.3	805	10	US-09-966-881-43
9	72.2	5.5	824	10	US-09-894-633A-83
10	70.2	5.3	1318	9	US-09-934-900-15
11	69.4	5.3	299	10	US-09-294-093B-3520
12	68	5.2	804	10	US-09-966-881-40
13	68	5.2	1415	9	US-09-934-900-11
14	66.8	5.1	4810	9	US-10-138-221-6
15	66.6	5.1	826	10	US-09-966-881-41
16	63.8	4.9	2712	10	US-09-748-033-4
17	60.2	4.6	2442	10	US-09-815-242-4030
18	60	4.6	1896	9	US-10-124-880-15
19	59.4	4.5	3430	9	US-10-163-214-1

20	57.6	4.4	3468	9	US-09-988-462-2
21	56.4	4.3	240	10	US-09-294-093B-3300
22	56.4	4.3	1164	10	US-09-815-242-7696
23	56.4	4.3	2622	10	US-09-815-242-7871
24	56.2	4.3	1226	9	US-09-764-891-10144
25	56	4.3	2331	10	US-09-815-242-4037
26	55.8	4.2	3153	10	US-09-922-501-13
27	55.6	4.2	1298	10	US-09-925-300-682
28	55.6	4.2	6252	10	US-09-964-824A-313
29	55	4.2	3386	9	US-10-163-214-11
30	55	4.2	88421	9	US-09-976-059-1
31	54.8	4.2	437	10	US-09-739-438-1
32	54.8	4.2	15872	9	US-09-860-846-1
33	54.8	4.2	15872	9	US-09-988-384B-1
34	54.8	4.2	15872	9	US-09-836-821-1
35	54.8	4.2	15872	9	US-09-861-289-1
36	54.6	4.2	3300	10	US-09-379-931-6
37	54.4	4.1	280	10	US-09-294-093B-1925
38	54.2	4.1	880	9	US-09-934-900-5
39	54.2	4.1	1467	10	US-09-981-900B-6
40	54.2	4.1	13842	9	US-09-860-846-30
41	54.2	4.1	13842	9	US-09-988-384B-30
42	54.2	4.1	13842	9	US-09-836-821-30
43	54.2	4.1	13842	10	US-09-861-289-30
44	54.2	4.1	36778	9	US-09-860-846-5
45	54.2	4.1	36778	9	US-09-836-821-5

ALIGNMENTS

RESULT 1

US-09-961-077-25
; Sequence 25, Application US/09961077
; Publication No. US20030014775A1

GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.
Edington, Brent E.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR
MODULATION OF GENE EXPRESSION
IN PLANTS

NUMBER OF SEQUENCES: 1263

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/961,077

FILING DATE: 21-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/679,645

FILING DATE: July 12, 1996

APPLICATION NUMBER: 60/001,135

FILING DATE: July 13, 1995

APPLICATION NUMBER: 08/300,726

FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 2267 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-961-077-25
Query Match 30.5%; Score 400.6; DB 9; Length 2267;
Best Local Similarity 60.0%; Pred. No. 1.5e-91;
Matches 810; Conservative 0; Mismatches 449; Indels 90; Gaps 5;
QY 5 TGGACATCGTATGGTTGCTGCTGAGGTGCGCCCTTGTGTCACAGACGGCGCCCTGGCGG 64
DB 418 TGAACGTGCTTCTGTCGGCGCCGAGATGGCGCGTGGAGCAAGACCGCGGCTTCGGCG 477
QY 65 AITGACGTGGTGGCTGCTATTGAGTGGTCAAGCGGGCCACCGCGTCATGACATTG 124
DB 478 AGTCTCTGGGGCTGCGCGCGGCATGGCGGGAATGGGCACCGTGTATGGTCTGCT 537
QY 125 CCGCTCGCTACGACAGTACGCTGACGCTGGGACACCTCGGTGGTGGTGGTGGACAT- 179
DB 538 CTCCCGCTACGACAGTACAGGACGCTGGACACCGCTGCTGCGGATCAAGA 597
QY 180 -----CATGGCGAGAGTCCGCTACTTCCATCCATCAAGAGGCGTGCACCGG 232
DB 598 TGGAGACAGTACAGAGCTGAGTCTTCTTCCACTGTACAGCGCGGAGTGGACCGG 657
QY 233 TGTGATTGACACCCCTGTTCTCTGGCCAGGTCTGGGCAAGACCGGCTCCAGCTGT 292
DB 658 TGTTCGTGACCCACCTGTTCTGGAGAGGTTTGGGAAGACCGAGAGAGATCT 717
QY 293 ACGGCCCGCTCGCGGCTGACTACCTGGGACACCAAGGCTTGGCCCTTGTGCA 352
DB 718 ACGGCTGAGCGTGAACGAGTACAGGACACAGCTGGGTTGAGCTGCTGATGCC 777
QY 353 AGCGCGTATTGAGGCTCGCGCTGCTGCTCGCCCTCGGC----- 390
DB 778 AGGAGCACTTGAAGCTCAAGGATCCCTGAGGCTCAACAAACCCATCTCTCGGAC 837
QY 391 --CCGGGAGAGTCCGCTCTGTTGGCCAGACTGGCACTCCGCCCTTGGTCCCGTCC 448
DB 838 CATACGGGAGGAGCTGCTGTTGCTGCTCAAGGAGTGCACACCGGCTCTCTGCTGT 897
QY 449 TCGTGAAGACAGTACAGCCAGGCGGAGTTCACCAAGCCAGTGGTGGTGGTGA 508
DB 898 ACCTCAAGAGCACTACAGTCCACGCGATCTACAGGAGCAGCAAGACCGTTCGCA 957
QY 509 TCCACACATCGCTTCCAGGCGCATGTGGGAGGAGGCTTTCAGGACACAGAGTGC 568
DB 958 TCCACACATCTCTTCCAGGCGCGGCTGCGCTTCTCGACTACCGGAGTGAACCTCC 1017
QY 569 CCCAGCGCGCTTTGACAGCTGGCTTCTCGAGCGGCTATGCCAAGGTTTACACTGAG 628
DB 1018 CGGAGATTCAGTCCGCTTCGATTTTCATCGACGGGTACGAGAAG----- 1064
QY 629 CCACCCCATGAGGAGGACGAGAGCCCGCTCAGCGGAAGACCTACAGAGATCA 688
DB 1065 -----CCCGTGAAG-----GCGGAGATCA 1086
QY 689 ACTGGCTGAAGGTGCAATTATCGCGCGGACAAAGTGTGACTGTGTGCGCCAACTAG 748
DB 1087 ACTGGATGAAGCGCGGATCTCTGAGGCGGACAGGCTCTCACCCTCAGCCCTACTAG 1146

RESULT 2

US-10-138-075-1
; Sequence 1, Application US/10138075
; Publication No. US20030087369A1
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Butler, Karlene H.
; APPLICANT: Harwell, Leslie T.
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Orozco, Emil M.
; TITLE OF INVENTION: Granule-Bound Starch Synthase
; FILE REFERENCE: BB1474 NA
; CURRENT APPLICATION NUMBER: US/10/138,075
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/288,315
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 2399
; TYPE: DNA
; ORGANISM: Zea mays
US-10-138-075-1

Query Match 18.7%; Score 245.6; DB 9; Length 2399;
Best Local Similarity 52.9%; Pred. No. 1.3e-52;
Matches 715; Conservative 0; Mismatches 544; Indels 93; Gaps 5;
QY 1 GCGTGGACATCGTATGTTGCTGCTGAGTGGCGCCCTTGTGTCACAGAGCGGCGCTG 60
DB 503 GGGATGACTATTGTTATTTGTTGCACTGAAGTGCACCCCTGTTGCAAACTGGTGGCCTC 562

FEATURE:

```

NAME/KEY: CDS
LOCATION: 3..2017
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-952-677-1

```

Query Match	8.9%	Score 116.8	DB 10	Length 2239
Best Local Similarity	52.4%	Pred. No. 3.2e-20		
Matches 331	Conservative 0	Mismatches 292	Indels 9	Gaps 3
QY	686	TCAACTGGGTGAAGGGTGGCATTATCCGCGCGACAAAGCTGGTACTGTGTGCCCAACT	745	
DB	823	TTAACATTTTGAAGAGGACAGTTGTGACAGCAGATCGGATTTGGACCGTCAGTCAGGGT	882	
QY	746	ACGGACCGAGATC----GCTGCCGATGCCCGCGGTGTGGAGCTGGACACCGTCATCC	802	
DB	883	ATTTCATGGGAGGTCACAACTGCTGAAGGTGGACAGGGCCTCAATGAGCTCTTAAAGTCCC	942	
QY	803	GCGCCAAGGSCATTGAGGGCATTGTGAAGGCGATGGACATTTGAGGAGTGGAAACCCCAAGA	862	
DB	943	GAARAAAGTGATTCAATGGAATTTGAATGGAATTCACATTAATGATGGAACCCCAACA	1002	
QY	863	CCGACAAGTTCCTGTGTGGCCCTACACACAGAACAGCTCTACGCCGGAAGGCGCGCG	922	
DB	1003	CAGACAAGTGTCTCCCTCATCATTAATTTCTGTCATGACCTCT---CTGGAAGAGCCAAAT	1059	
QY	923	CCRAGAGGCCCTGCAGCGCGAGCTGGGCTGCTGTGGACCCACCGCCGCCCTGTTCG	982	
DB	1060	GTAAGCTGAATTTGCAGAAGAGTGGTTTACCTGTGAGGGAGGATGTTCTCTGATTG	1119	
QY	983	CCTTCATCGCCGCCCTGGAGGACGAAGGGTGTGACATCATCTCTGGCGGCCCTGCCCA	1042	
DB	1120	GCITTTATTGGAAGACTGGATTACAGAAAGGCCATTGATCTCAATAAAATGGCCATTCAG	1179	
QY	1043	AGATCTGGCCACCCCAAGTGCAGATCCCATCTGGTACCGGCAAGGCGCGCTACG	1102	
DB	1180	AGCTCATG---AGGGAGGAGTGCATTTCTCATGCTTGGATCTGGGGATTCCAATTTTG	1236	
QY	1103	AGAAGCTGGTGAACGCCATCGGACCAAGTACAAGGCGCGCCGACAGGGCGTGGTCAAGT	1162	
DB	1237	ANGCTGGATGAGATCTACCGAGTCGAGTTACAAGGATAAATTCGCTGGATGGTTGGAT	1296	
QY	1163	TCTGGCGGCCCTGGCGGCACATGCTACCGCGCGCGCGACTTCATGCTGGTGGCCTHCG	1222	
DB	1297	TTAGTGTTCAGATTTCACAGATAAATTCAGGTTGCGATATATTGTTAATGCCATPCGA	1356	
QY	1223	GCTTCGAGCCCTCGGGCTCATCCAGCTGCACGCCATGCGACTACGGTACCGTGCCTGG	1282	
DB	1357	GATTTGAACCTTCGGGTCTTAATCAGCATATATGCTATGCAATATGGTACAGTCTCTGTAG	1416	
QY	1283	TAGCCTCCACGGCGGCTGGTGGACACCGTC	1314	
DB	1417	TTCATGGAACCTGGGGGCTCCGAGACAGATC	1448	

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/966,881
  FILING DATE: 28-Sep-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/242,860
  FILING DATE: 29-Mar-1999
  APPLICATION NUMBER: GB 9618862.8
  FILING DATE: 10-SEP-1996
  APPLICATION NUMBER: GB 9708366.1
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: PCT/GB97/02424
  FILING DATE: 08-SEP-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Hohenschutz, Liza D.
  REGISTRATION NUMBER: 33,712
  REFERENCE/DOCKET NUMBER: SEE 50183/UST
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (302) 886-1699
  INFORMATION FOR SEQ ID NO: 44:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 790 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: unknown
      MOLECULE TYPE: CDNA
      IMMEDIATE SOURCE:
        CLONE: U-D111
        SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-966-881-44

```

		7.2%;	Score 94.2;	DB 10;	Length 790;		
Query Match		57.2%;	Pred. No. 1.5e-14;				
Best Local Similarity		Conservative 0;	Mismatches 144;	Indels 13;	Gaps 2;		
Matches 210;							
QY	1	GC	GTGACATCGTGATGGTTCGTCTGAGTTCGCCCTTTGGTCCAAAGACGGCGCGCTG	60			
Db	310	GG	GATGAACATAGCTTTTGTCTGGCGCTGANATGCCTCCCTGGAGTAATAAACCGGAGGACTC	369			
QY	61	GG	CATGTGACTGTGTGGCTGCCTATTGAGCTGGTCAAGCGCGCCACCCTCATCAACC	120			
Db	370	GG	TGAIGTCTTGTGAGGACTGCCACCGCCATGGCTGCAAAATGGACACACAGTAGTACT	429			
QY	121	ATT	CGCCCTCGCTACGACCACTGACGTGACGSCCTGGGACACCTCGGTGGTGGACATC	180			
Db	430	ATA	GCTCCACCTATGATCATGATCAAGATGGGTGGATACAATGCTCTGGCTGAGTTA	489			
QY	181	AT	GGCGGAGAGG-----TCGCTACTTCCACTCCATCAAGAAGGGCGTGCAC	238			
Db	490	AAA	GTTGGAATGAAATTTGAAAGANTCGGCTCTCTCCACTGCTATAAAAGAAGANTTGAC	549			
QY	229	CG	GTGTGGATGACCAACCCCTGGTCTCTGCCCAGAGTCTGGGCGCAACCGCTCCAAG	288			
Db	550	AG	GTTTTTCATTGATCATCTCTTTTCTTGANAAGGTGTGGGAAACAACTGGGAAGATG	609			
QY	289	CT	GTACGGCCCCG--CTCCGGCGCTGACTACTCTGGACAACCAACCAAGCGCTTCGCCCTGTT	347			
Db	610	ATA	TATGTCCTCTCNCAGGACNGATTATGAANACCAACCACTAAGATTAACTTTTG	669			
QY	348	CT	GCAAG 354				
Db	670	TT	GCAG 676				

RESULT 9

US-09-894-633A-83
; Sequence 83, Application US/09894633A
; Patent No. US20020124285A1

GENERAL INFORMATION:

; APPLICANT: Conner, Timothy
; APPLICANT: Dubois, Patricia
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSION
; FILE REFERENCE: 38-21(15856)B
; CURRENT APPLICATION NUMBER: US/09/894,633A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/214,357
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 09/894,633
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.0

SEQ ID NO 83

LENGTH: 824

TYPE: DNA

ORGANISM: Zea mays

US-09-894-633A-83

Query Match

Best Local Similarity 5.5%; Score 72.2; DB 10; Length 824;

Matches 246; Conservative 0; Mismatches 268; Indels 3; Gaps 1;

QY 795 CGTCATCCGCGCCGAAGGCGATTTGAGGCGATTTGTAACGGCATGGACATTTGAGGAGTGA 854
DB 132 CCGTCCGCGCTTTCTTCCAGACTGCTTCTCAGCGGGTTCGACGGTCTGGTCTGTAT 191
QY 855 CCCCAGACGACAGATTCCTGTCTGCGCCCTACACGACAGACGCTCTACGCGGCAA 914
DB 192 CGGFTCCACAGTTCGAGAGTCGGAGCACACCGGGAGATCAACCACTCCCTCCCGG 251
QY 915 GSCCCGCCCAAGGAGGCGCTGCAGGCGGAGTGGCGCTTGCCTGTGGACCCCGCCGCC 974
DB 252 GGACGCTTCGACGCGGTTGGTGCAGCGCCCAAGCTGGCCCTGGAGCTGGAGTGCCTGG 311
QY 975 CCGTGTCCGCTTCATCGGCGCGCTGGAGAGCAGAGGTTGTGGACATCATCTGCGCGC 1034
DB 312 GGTGT---CCTGCGCGCATCTCTCGCATGCGCTGCGGCGTGTGTATACCATGACCGG 368
QY 1035 CCGTCCCAAGATCTCTGGCCACCCCAAGGTGCAGATCGCATCTCTGGGTACCGCAAGC 1094
DB 369 CGGCGCCCGGTACCCGGTTCGCTGGGGCGAGGACTCGCTGTCTGTCGCCACCGC 428
QY 1095 CGCCTACGAGAGCTGGTGAACGCCATCGGCACCAAGTACAAAGGCGCGCCCAAGGCGT 1154
DB 429 GCGCGACGTGGAGCTGCCGACGCGCAACTTCACCGTGGACCGCTCATCCAGATGTCG 488
QY 1155 GGTCAAGTCTCGGCGCGCTGGCGACATGCTACCGCGCGCGGAGCTTATGCTGT 1214
DB 489 CGCCAAAGGGTTACGCGTGCAGAGAGTGGTGGCGTGTCCGCGCCACACGCTGGGTT 548
QY 1215 GCGCTCGCGTTCGAGCGCTGCGGCTGTATCCAGTGCACGCGATGCACTAGCGTACC 1274
DB 549 CTCCCACTGCAAGAGTTCGCGGACCGGCTCTACACTTCCCAACAGGCGGGNAGCC 508
QY 1275 GCGCGTGGTAGCTCCACCGCGGCGCTGGTTCGACACC 1311
DB 609 GGAGCAGTTCGACCCCGCAGCATGAACCGGTCCTACGCC 645

RESULT 10

US-09-934-900-15
; Sequence 15, Application US/09934900
; Publication No. US20030054521A1

GENERAL INFORMATION:

; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E

; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearo
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1318
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-09-934-900-15

Query Match

Best Local Similarity 5.3%; Score 70.2; DB 9; Length 1318;

Matches 261; Conservative 0; Mismatches 318; Indels 0; Gaps 0;

QY 713 CGCGCGACAAGCTGGTGTCTGCGCCCAACTACGCGACCGAGATCGCTGCGGATGCGG 772
DB 286 CGGACTTCTCGCGGACTCGTCTCGGAGATGTTGAGCACCAGGTTCACGAGCTCCGCG 345
QY 773 CGCGGGGTGTGAGCTGGACACCGCTCATCCGGGCCAAGGCGCATTTAGAGGCATTTGAACG 832
DB 346 CGCGCGCGCGGGCTCCCGCGACGAGTACTTCTGCTGTGTTGCGGGGATGATTACCG 405
QY 833 GCATGACATTTAGAGTGGACCCCAAGACCGACAGATTCCTGTCTGCGCCCTAGCAC 892
DB 406 AGGAGCGCTGCGCGAGTACACCATGATCAACACGCTGACGCGCTCCGCGAGAGA 465
QY 893 AGAACAGCGTCTACGCGCGCAAGGCGCGCCCAAGGAGCGCTGACAGCGCGAGCTGGCG 952
DB 466 CGCGGCCAGCGCTGCCCTCGGCGCTGTGACGCGCCTGAGCGCGACCTGGAGCGCGAGGAAC 525
QY 953 TGCTGTGACCCCGCCCGCTGTTGCGCTTCTATCGCGCGCTTGGAGGAGCAGAGG 1012
DB 526 GCCAGCGGACATCTCTCGGCAAGTACATCTCTCCGCGCGCTGACATGCGCATGG 585
QY 1013 GTGTGACATATCTGCGCGCGCTGCTGCCCAAGATCTTGGCACCACCGAGGTGACATCG 1072
DB 586 TGAGAGAGACCTCCAGTACCTCATCGCTCCGCGCATGATCGGGAGCGGAGAGCAACC 645
QY 1073 CCATCTGTGTACCGCGCAAGGCGCTACGAGAGCTGTGTAACGCGCATCGGCAACAGT 1132
DB 646 CGTACCTGGGTTCTGTGTAACAGCTTCCAGAGCGCGGCGCGCTGTGCGACGGA 705
QY 1133 ACAAGGCGCGCCCAAGGCGGTGTCAAGTTCCTGCGCGCGCTTGGCGCACATGCTCACCG 1192
DB 706 ACAGCGCGCTTCGCGAGGCGCGACGGGAGACGCTCTGCGCGCGCACCTGCGGCA 765
QY 1193 CGGCGCGCACTGCTGTGCTGCGCTTCCGCTTCCAGCCCTGCGCGCTGATCCAGTGC 1252
DB 766 TCGCGCGCGCGAGAGCGCGACGAGACGCGCTTACGCGCGCATCTGTGGAGCAGCTGCTG 825
QY 1253 AGCCCATGCACTACGCTACGCTGCGCGGTGTGATGCTCCCA 1291
DB 826 GCGTCAACCGGACGCGCGCATGCTGCGCATGCCGACA 864

RESULT 11

US-09-294-093B-3520
; Sequence 3520, Application US/09294093B
; Patent No. US20010051335A1

GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US


```
QY 120 CATTGCCCTCGCTACGACACAGTACGCTGACGCCCTGGACACACCTCGGTGGTCTGGACAT 179
Db || || || || || || || || || || || || || || || || || || || || ||
427 TATAGTCCACGCTATGATCAGTACAGGATGGGTGGGATACAAATGTCTCTGGCTGANIT 486
QY 180 CATGGCGGAGAAGG-----TCGGCTACTTCCACTCCATCAAGAAGGGCGTGCA 227
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
487 AAAAGTTGGAATGAAATTCAGAGAATCCGCTTCTTCCACTGTATNAANAAGAAITGA 546
QY 228 CCGCGTGTGGATTGACCA-CCCGTGTCTCTGGCCCAAGGTCTGGGGCAAGACCGGCTCCA 286
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
547 CAGGGTTTTCATTGATCATCCTTTGTTTCTTGAAAANGTGTGGGAAAACACTGGANGAA 606
QY 287 AGCTGTACGGCCCCCGCTCGGGCGCTGACTA 317
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
607 TGATAINTGCTCTGTCCNGGAACGGATTA 637
```

Search completed: June 6, 2003, 22:50:16
Job time : 135.284 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 13:49:45 ; Search time 23.2306 Seconds
(without alignments)
2512.365 Million cell updates/sec

Title: US-09-980-771A-7

Perfect score: 2288

Sequence: 1 ALDIVMAAEVAPWSKTGGL.....AMHYGIVPVVASGGLVDTV 438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1257.5	55.0	606	AA25476	Granule-bound star
2	1249.5	54.6	502	AA25474	Central fragment f
3	1242	54.3	527	AA25473	Arabidopsis thalia
4	1242	54.3	563	AA25472	Arabidopsis thalia
5	1242	54.3	610	AA25471	Arabidopsis thalia
6	1242	54.3	610	AA25470	Arabidopsis thalia
7	1229	53.7	609	AA25469	Herbicidally activ
8	1185	51.8	533	AA25468	Oryza sativa starch
9	1176	51.4	637	AA25467	Zea mays waxy gene
10	870	38.0	626	AA25466	Protein encoded by
					Soluble rice starch

11	862	37.7	647	20	AA25465	Wheat starch solub
12	862	37.7	671	19	AA25464	Wheat soluble star
13	862	37.7	756	21	AA25463	Wheat soluble star
14	861	37.6	649	19	AA25462	Maize starch synth
15	859	37.5	539	19	AA25461	Zea mays starch sy
16	859	37.5	583	19	AA25460	Zea mays soluble s
17	856	37.4	792	23	AA25459	Herbicidally activ
18	850	37.2	583	23	AA25458	Herbicidally activ
19	846.5	37.0	652	23	AA25457	Maize starch solub
20	817	35.7	799	19	AA25456	Wheat granule-boun
21	816	35.7	802	23	AA25455	Modified barley st
22	816	35.7	813	23	AA25454	Barley cultivar Mo
23	815	35.6	812	23	AA25453	Barley line MK6827
24	813	35.5	798	21	AA25452	Wheat starch synth
25	813	35.5	799	21	AA25451	Wheat starch synth
26	813	35.5	799	21	AA25450	Wheat starch synth
27	810	35.4	698	19	AA25449	Zea mays soluble s
28	810	35.4	804	19	AA25448	Maize starch solub
29	801	35.0	597	21	AA25447	Wheat starch synth
30	794.5	34.7	812	23	AA25446	Barley line 292 st
31	762.5	33.3	534	21	AA25445	Wheat starch synth
32	719	31.4	466	23	AA25444	Rice starch synth
33	696	30.4	459	17	AA25443	Soluble starch syn
34	671.5	29.3	669	19	AA25442	Maize starch solub
35	671.5	29.3	669	19	AA25441	Zea mays soluble s
36	622.5	27.2	476	23	AA25440	Streptococcus poly
37	601	26.3	483	23	AA25439	Lactococcus lactis
38	558	24.4	477	13	AA25438	glgA, Escherichia
39	558	24.4	477	19	AA25437	E. coli glycogen s
40	528	23.1	735	18	AA25436	Z. mays starch syn
41	528	23.1	677	17	AA25435	Soluble starch syn
42	528	23.1	1230	18	AA25434	Potato tuber solub
43	528	23.1	1230	21	AA25433	Potato starch synt
44	520	22.7	495	19	AA25432	Protein encoded by
45	520	22.7	1025	23	AA25431	Herbicidally activ

ALIGNMENTS

RESULT 1
AA25476
ID AA25476 standard; Protein; 606 AA.
XX
AC AA25476;
XX
DT 15-JAN-1993 (first entry)
XX
DE Granule-bound starch synthase of potato.
XX
KW GBSS gene; amylopectin; amylose production;
inhibition; promoter; antisense construct.
XX
OS Solanum tuberosum.
XX
PN WO9211376-A.
XX
PD 09-JUL-1992.
XX
PF 20-DEC-1991; 91WO-SE00892.
XX
PR 21-DEC-1990; 90SE-0004096.
XX
PA (AMYL-) AMYLOGENE HB.
XX
PI Hofvander P, Persson PT, Tallberg A, Wikstrom O;
XX
DR WPI; 1992-250096/30.
XX
N-PSDB; AAQ26404.
XX
PT Modifying potatoes to form amylopectin starch - using an
anti-sense construct to inhibit granule-bound starch synthase

PS Claim 6; Page 28-33; 46pp; English.

XX A genomic library in EMBL3 was prepared using leaves of the potato
 CC Bintje. The library was screened with cDNA clones for the 5' and 3'
 CC ends of the GBSS gene. A full-length clone of potato GBSS gene was
 CC identified (wx311) and isolated from the genomic library. The gene
 CC contained 12 introns. The amino acid sequence was deduced from it.
 CC Three fragments of the full-length sequence (5'-end, middle and
 CC 3'-end sequences) were characterised as suitable for use in novel
 CC antisense constructs to suppress amylose formation in potatoes.
 CC See also Q26400-3.

XX SQ Sequence 606 AA;

Query Match 55.0%; Score 1257.5; DB 13; Length 606;
 Best Local Similarity 55.7%; Pred. No. 3.8e-105; Indels 31; Gaps 7;
 Matches 250; Conservative 54; Mismatches 114;

QY 2 LDIVVMAAEVAPWSKTGGLDVTGGLPIELVKRGRHVMITAPRYDQYADAWDTSVVVDI- 60
 DB 81 MNLIFVGTGVPWSKTGELGGLGGLPPLAARGHVMITSPRYDQYKDAWDTGVAVEVK 140

QY 61 MG---EKVRYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRFALFC 117
 DB 141 VGDSEIEIVRFHCHYKRGVDFVDPHMFLEKVGKTSKIYGPAGLDYLDNHRFSLLC 200

QY 118 KAATEAARVLFP-----GP-GEPCVFVANDHVSALVPVLLKDEYOPKQFTKAKSVLA 169
 DB 201 QAALAPKVLNLSNNTSFSGYGEDVLFANDHWTALIPCYLKSMTYQSGIYLNKAVFC 260

QY 170 IHNIAFGRMWEAEAFKDKLPQAADFKLAFSDGYAKVYVTEATPMEDEKPLTGTGTYKKI 229
 DB 261 IHNIAYGQRFSEFDFLNLDPDEFKSGDFIDGY-----KPVKG---RKI 302

QY 230 NWLKGGLIADKLVTSVSNYATETAADAGGVELDTVIRAKGIEGIVNGMDIEEWNPKTD 289
 DB 303 NNMKAGILESHRVVTVSPYTAQELVSAVDKGVELDSVLRKTCITGIVNGMDTQEWNPATD 362

QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFIFGRLEEQGVDIILALPKI 349
 DB 363 KYTDVKYDITVMDAKPLKLEALQAAVGLPVDKKIPLIGFIFGRLEEQKGSIIIVAAIHKF 422

QY 350 LATPKVQIAILGTGKAAAYEKLIVNAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSRF 409
 DB 423 IGL-DVQIVVLGTGKKEFEQIEOLEVLYPNKAKGVAKFNVPPLAHMITAGADFMVPSRF 481

QY 410 EPCGLIOLHAMHYGTVPVASTGGLVDTV 438
 DB 482 EPCGLIOLHAMRYGTVPICASTGGLVDTV 510

RESULT 2
 AAR25474
 ID AAR25474 standard; Protein; 502 AA.
 XX AC AAR25474;
 XX DT 15-JAN-1993 (first entry)
 XX DE Central fragment from potato GBSS.
 XX KW Granule-bound starch synthase; amylopectin; amylose production;
 XX OS inhibition.
 XX OS Solanum tuberosum.
 XX FN W09211376-A.
 XX PD 09-JUL-1992.
 XX PF 20-DEC-1991; 9LWO-SE00892.
 XX PR 21-DEC-1990; 90SE-0004096.

XX (AMYL-) AMYLOGENE HB.
 XX Hofvander P, Persson PT, Tallberg A, Wikstrom O;
 XX WPI; 1992-250096/30.
 XX N-PSDB; AAQ26401.
 XX Modifying potatoes to form amylopectin starch - using an
 XX anti-sense construct to inhibit granule-bound starch synthase
 XX Claim 1; Page 21; 46pp; English.

XX A genomic library in EMBL3 was prepared using leaves of the potato
 CC Bintje. The library was screened with cDNA clones for the 5' and 3'
 CC ends of the GBSS gene. A full-length clone of potato GBSS gene was
 CC identified (wx311). A BglII-SpeI fragment ("m") of the clone was
 CC found to contain the central region of the gene and was cloned in
 CC pUC13 to give pSm. Restriction of pSm with NsiI and HpaII gives
 CC fragment II which was cloned in pURD184 to give pURDm11. Further
 CC restriction of pURDm11 with HpaI-SstI gives a 2549bp fragment
 CC comprising exons and introns from the middle of the gene. The
 CC fragment can be used to make antisense constructs to suppress amylose
 CC formation in potatoes. See also Q26400-4.

XX SQ Sequence 502 AA;

Query Match 54.6%; Score 1249.5; DB 13; Length 502;
 Best Local Similarity 55.6%; Pred. No. 1.6e-104; Indels 33; Gaps 8;
 Matches 250; Conservative 53; Mismatches 114;

QY 2 LDIVVMAAEVAPWSKTGGLDVTGGLPIELVKRGRHVMITAPRYDQYADAWDTSVVVDI- 60
 DB 39 MNLIFVGTGVPWSKTGGLDVTGGLPPLAARGHVMITSPRYDQYKDAWDTGVAVEVK 98

QY 61 MG---EKVRYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRFALFC 117
 DB 99 VGDSEIEIVRFHCHYKRGVDFVDPHMFLEKVGKTSKIYGPAGLDYLDNHRFSLLC 158

QY 118 KAATEAARVLFP-----GP-GEPCVFVANDHVSALVPVLLKDEYOPKQFTKAKSVLA 169
 DB 159 QAALAPKVLNLSNNTSFSGYGEDVLFANDHWTALIPCYLKSMTYQSGIYLNKAVFC 218

QY 170 IHNIAFGRMWEAEAFKDKLPQAADFKLAFSDGYAKVYVTEATPMEDEKPLTGTGTYKKI 229
 DB 219 IHNIAYGQRFSEFDFLNLDPDEFKSGDFIDGY-----KPVKG---RKI 259

QY 230 NWLKGGLIADKLVTSVSNYATETAADAGGVELDTVIRAKGIEGIVNGMDIEEWNPKTD 289
 DB 260 NNMKAGILESHRVVTVSPYTAQELVSAVDKGVELDSVLRKTCITGIVNGMDTQEWNPATD 319

QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFIFGRLEEQGVDIILALPKI 348
 DB 320 KYTDVKYDITVMDAKPLKLEALQAAVGLPVDKKIPLIGFIFGRLEEQKGSIIIVAAIHK 379

QY 349 ILATPKVQIAILGTGKAAAYEKLIVNAIGTKYGRAGVVKFSAPLAHMLTAGADFMVPSR 408
 DB 380 FIGL-DVQIVVLGTGKKEFEQIEOLEVLYPNKAKGVAKFNVPPLAHMITAGADFMVPSR 438

QY 409 EPCGLIOLHAMHYGTVPVASTGGLVDTV 438
 DB 439 EPCGLIOLHAMRYGTVPICASTGGLVDTV 468

RESULT 3
 AAG04668
 ID AAG04668 standard; Protein; 527 AA.
 XX AC AAG04668;
 XX DT 17-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 782.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127482.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137582.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.

```
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 54.3%; Score 1242; DB 21; Length 527;
Best Local Similarity 55.3%; Pred. No. 8e-104;
Matches 250; Conservative 59; Mismatches 107; Indels 36; Gaps 9;

QY 2 LDIVAAAEVAPWSKTGGLGVTGGLPLTVKRGHRVMTIAPRYDQYADANDTSVVDI- 60
Db 1 MSVFIGAEVGPWSKTGGLGVLGGLPALAARGHRVMTICPRYDQYKDAWDTCVVOIK 60
QY 61 MGEK---VRYPHSTKKGVHRWIDHPWFLAKVWGKTGSKLYCPRGADYLDNHKRFALPC 117
Db 61 VGDKVENRPFHCYKRGVDRVFDHPFLAKVVGKTGSKYKIPITGVVDYNDNQLRFLSLIC 120
QY 118 KAALEAAARVLFP-----GP-GDCVFEVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA 169
Db 121 QAALEAPVNLNNSKYSFGYGEDVFEVANDWHTALLPCYLSMIQSRGVTMNAKVFC 180
QY 170 IHNIAFGRMWEAFKDTKLFP---QAADFKLAFSDGYAKVYTEATPFMEDEKPLTGTXY 226
Db 181 IHNIAYGRAFDYDLSLNLPIFSKSPD---FMDGYEK-----PVKG--- 220
QY 227 KKNLWKGIIAUAUKLVTVSNYATEAADAAGGVVELDTVIRAKGIEGVINGMDTEENWP 286
Db 221 KKNWKAAILFAHRLVSPYQAQELISGVDGRGVGLHKLRMKTVSGIINGMDVOEWNP 280
QY 287 KTDKLSAPYDQNSYAGKAAKALQALQELPVDPTAPLFAFIFGRLEEQKGVDIILAL 346
```

```
Db 281 STDKYIDIKYDITITVDKAPLIKEALQAAVGLPVRDREVEVIGFIRLEEQKGSILVEAI 340
QY 347 PKILATPKVQIAILGTGKAAVEKLYNAIGTKYKGRAGVWVFESAPLAHMLTAGADFMVLP 406
Db 341 SKFMGL-NVQWVILGTGKKKEAQILEEKEFGKAVGVKFNVPFLAHMITAGADFIIVP 399
QY 407 SRFEPGLIQLHAMHYGIVPVVASTGGLVDTV 438
Db 400 SRFEPGLIQLHAMRYGTVPVIVASTGGLVDTV 431
```

RESULT 4

AAG04667

ID AAG04667 standard; Protein; 563 AA.

XX AAG04667;

XX

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 781.

XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132484.

XX 06-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 07-MAY-1999; 99US-0132487.

XX 11-MAY-1999; 99US-0132863.

XX 14-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134219.

XX 14-MAY-1999; 99US-0134221.

XX 18-MAY-1999; 99US-0134370.

XX 19-MAY-1999; 99US-0134768.

XX 20-MAY-1999; 99US-0134941.

XX 21-MAY-1999; 99US-0135124.

XX 24-MAY-1999; 99US-0135353.

XX 25-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136392.

XX 28-MAY-1999; 99US-0136782.

XX 01-JUN-1999; 99US-0137222.

XX 03-JUN-1999; 99US-0137528.

XX 04-JUN-1999; 99US-0137502.

XX 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139453.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140931.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143325.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145911.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
PR 01-SEP-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155139.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 54.3%; Score 1242; DB 21; Length 563;
Best Local Similarity 55.3%; Pred. No. 8.8e-104;
Matches 250; Conservative 59; Mismatches 107; Indels 36; Gaps 9;

PR 12-SEP-1997; 97AU-0009108.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (GOOD-) GOODMAN FIELDER LTD.
 PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
 XX (AUSU) UNIV AUSTRALIAN NAT.
 PI Li Z, Morell M, Rahman S;
 XX WPI; 1999-229525/19.
 DR N-PSDB; AAX34651, AAX34652.
 XX
 PT New isolated cereal plant enzyme genes used for, e.g. expression of
 PT antisense sequences of granule bound synthase
 XX
 PS Claim 13; Page 95-97; 17lpp; English.
 XX
 CC The invention relates to a novel enzyme of starch biosynthetic pathway
 CC in a cereal plant, where the enzyme is selected from starch branching
 CC enzyme (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching
 CC enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or
 CC SBE I of rice or maize. The methods and products can be used for
 CC targeting expression specifically to the endosperm of the seeds of cereal
 CC plants such as wheat or barley. They can be used for the expression of
 CC e.g. antisense sequences of granule-bound synthase (GBSS), SBE II, low
 CC mol. wt. glutenin, grain softness protein I, bacterial isoamylase,
 CC bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They
 CC can be used for modifying the characteristics of starch produced by a
 CC plant. The present sequence represents the wheat SSS I protein sequence.
 XX
 XX Sequence 647 AA;
 PS Query Match 37.7%; Score 862; DB 20; Length 647;
 PS Best Local Similarity 43.1%; Pred. No. 3.1e-69;
 PS Matches 194; Conservative 70; Mismatches 148; Indels 38; Gaps 12;
 QY 4 IVMAAEVAPWSKTKGLDVTGGPIELVKRGHRVMTAPRY-----DQYADAWDTSVV 57
 DB 141 IVFTVGEAAPYAKSGGLDVCGLPIALAAARGHRVVMVPRYLNGSSDKNTAKALYTKGH 200
 QY 58 VDIM----GEKRVFHSIKKGVRWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNKHRE 113
 DB 201 IKIPCFGSGHEVTFEYRDNDVWVFDHP-----SYHRPGS-LYGNDFGA-FGDNQRY 253
 QY 114 ALFCKAAEAARVLFPFGP---GECVFVANDWHSALVPVLKDYQPKGQFTKAKSLAI 170
 DB 254 TLLCYAAACEAPLILELGGYIYGQNCMFVNDWHSALVPVLLAAKRYRPGVYVDRSRLTVI 313
 QY 171 HNIAFQGRMWEAEAFKDKLPQAAFDKLAFLSDGYAKVYVTEATPMEDEKPLTGTYYKIN 230
 DB 314 HNLHQGLEPASTYDGLPEWYGALEW-----VPEWARRIALDKG-----EAVN 360
 QY 231 WLKGGIIAOKLVTVSNYAFETIADAAGGVYELDTVI--RAKGIEGVINGMDIEBWNPKT 288
 DB 361 FLKGVAVTADRVTVSQYCSMEVTT-AEGGQGLNELLSSRKSVLNGIVNGIDINDWNPTT 419
 QY 289 DKFLSAPYQNSVYAGRAAKAEALQAEGLPVDPTAPLFAFIEGLEQKGVDDIILALPK 348
 DB 420 DKCLPHYVSDDL-SGAKCKAEALQELGLPVEDVPLIGFIRLDYQKGLDLKMAIPE 478
 QY 349 ILAIPKQVQIALIGTGKAYEKLVAIGTKYGRKGVVVKFSAPLAHMLTAGADEMLVPSR 408
 DB 479 LM-REDVQFVMLGSGDPTFEQWMSRSTESSYKDKRGVGVFVSPVSHRITAGCDILLMPSR 537
 QY 409 FEPGLIQLHAMHYGTVPVVAASVSTGGLVDTV 438
 DB 538 FEPGLNOLYAMQYGTVPVVGHTGGLRDTV 567
 RESULT 12
 AAW23937
 ID AAW23937 standard; Protein; 671 AA.
 XX

AC AAW23937;
 XX 21-MAY-1998 (first entry)
 XX Wheat soluble starch synthase partial sequence.
 DE Starch synthase; wheat; transgenic plant.
 XX Starch synthase; wheat; transgenic plant.
 XX Triticum aestivum L. cv. Florida.
 OS WO9745545-A1.
 PN 04-DEC-1997.
 XX 28-MAY-1997; 97WO-EP02793.
 PR 11-SEP-1996; 96DE-1036917.
 PR 29-MAY-1996; 96DE-1021588.
 XX (AGRE) HOECHST-SCHERING AGREVO GMBH.
 PA Block M, Loerz H, Luetticke S, Froberg C, Kossmann J;
 PI Walter L;
 XX WPI; 1998-032652/03.
 DR N-PSDB; AAV01527.
 XX
 PT Nucleic acid encoding starch synthase enzymes from wheat - for
 PT transgenic plants that produce modified forms of starch, useful e.g.
 PT in foods, or for production of packaging materials and disposable
 PT goods
 XX
 PS Claim 1; Page 47-50; 7lpp; English.
 CC This amino acid sequence comprises a near full-length sequence for
 CC a soluble starch synthase of summer wheat (cv. Florida). It was
 CC deduced from a cDNA clone (AAV01527) isolated from a 21-day caryopsis
 CC cDNA library. A granule-bound starch synthase (see AAW23938) has
 CC also been identified. Isolated nucleic acids encoding these
 CC enzymes can be inserted into vectors for production of transgenic
 CC plants, particularly starch-producing plants, specifically wheat.
 CC Use of the isolated nucleic acids, or of antisense sequences, allows
 CC starch metabolism to be regulated in transgenic plants.
 CC Overexpression may result in improved crop yield, while modification
 CC of starch in planta may eliminate the need for subsequent
 CC chemical/physical modification. Plants with altered levels of the
 CC various isoforms of starch synthase will produce starch of different
 CC chain length, amylose/amylopectin ratio, degree of branching,
 CC phosphate content, gelatinisation behaviour, granule size and shape,
 CC viscosity etc. The starch produced by such plants is useful
 CC particularly in foods (especially bakery goods or pasta) or to
 CC produce packaging materials or disposable goods, as well as in any
 CC other known use of starch.
 XX
 SQ Sequence 671 AA;
 Query Match 37.7%; Score 862; DB 19; Length 671;
 Best Local Similarity 43.1%; Pred. No. 3.2e-69;
 Matches 194; Conservative 71; Mismatches 147; Indels 38; Gaps 12;
 QY 4 IVMAAEVAPWSKTKGLDVTGGPIELVKRGHRVMTAPRY-----DQYADAWDTSVV 57
 DB 56 IVFTVGEAAPYAKSGGLDVCGLPIALAAARGHRVVMVPRYLNGSSDKNTAKALYTKAH 115
 QY 58 VDIM----GEKRVFHSIKKGVRWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNKHRE 113
 DB 116 IKIPCFGSGHEVTFEYRDNDVWVFDHP-----SYHRPGS-LYGNDFGA-FGDNQRY 168
 QY 114 ALFCKAAEAARVLFPFGP---GECVFVANDWHSALVPVLKDYQPKGQFTKAKSLAI 170
 DB 169 TLLCYAAACEAPLILELGGYIYGQNCMFVNDWHSALVPVLLAAKRYRPGVYVDRSRLTVI 228
 QY 171 HNIAFQGRMWEAEAFKDKLPQAAFDKLAFLSDGYAKVYVTEATPMEDEKPLTGTYYKIN 230

```

Db 229 HNLAHQGVPEASTYDPLGLPPEWYGALEW-----VFPEWARRHALDKG-----EAVN 275
QY 231 WLKGGITIAADKLVTSFSPNYATEIAAAGGVELDTVI--RAKGGIEGVNMGDIENPKT 288
Db 276 FLKAVVTADRIIVTSQGYSEWVIT-AEGGQGLNELSSRSKSVLNGVINGIDINDWNP 334
QY 289 DKFLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFVIGRLEBQKGVDIILALPK 348
Db 335 DKCLPHYSVDDL-SGKAKCAELQELGLPVREDVPLIGFVIGRLDYQKGLDLIKMAIPE 393
QY 349 ILATPKVQIAILGTGKAAYEKLVNAIGTKYKRAKGVVVKFSAPLAHMLTAGADEMLVPSR 408
Db 394 LM-REDVQFVNLGSGDPVIFEGWMRSTESSYKDKFRGWGFSVPVSHRITACGDIILLMPSR 452
QY 409 FEPGGLIQLHAMHYGTVPVVAAGGLVDV 438
Db 453 FEPGGLNQLYAMQYGTVPVVGHTGGLRDTV 482

```

RESULT 13

AAV50818
ID AAV50818 standard; Protein; 756 AA.

XX AC AAV50818;

XX DT 18-FEB-2000 (first entry)

XX DE Wheat soluble starch synthase protein.

XX KW Soluble; starch synthase; wheat; transgenic plant; starch production;
KW food; baking; pastry; packaging material; glucose; glucan; paper; pulp;
KW adhesive; textile; building material; soil stabilizer; wetting agent;
KW fertilizer; plant-protection; cosmetic; flocculant.

XX OS Triticum aestivum.

XX FN DE19820607-A1.

XX PD 11-NOV-1999.

XX PF 08-MAY-1998; 98DE-1020607.

XX PR 08-MAY-1998; 98DE-1020607.

XX PA (AGRE) HOECHST-SCHERING AGREVO GMBH.

XX PI Loerz H, Luetticke S, Block M;

XX DR WPI; 2000-024508/03.

XX DR N-PSDB; AA224487.

XX PT New enzyme with starch synthase activity, useful for producing starch
XX for foods and packaging materials -

XX PS Claim 1a; Page 19-21; 24pp; German.

XX CC This invention describes a novel protein (I) with the activity of wheat
XX starch synthase. Transgenic plants, specifically wheat, that contain (I)
XX are used for production of starch, used particularly in foods,
XX particularly baked and pastry goods and for making packaging materials or
XX disposable items. Starch may also be used as starting materials for
XX glucose or glucan components (e.g. for fermentation or further chemical
XX conversion); in paper and pulp production, as adhesives, in textiles,
XX in preparation of gypsum-based building materials, as soil stabilizer,
XX as wetting agent etc. in fertilizer and plant-protection compositions,
XX as binder (in pharmaceuticals, cosmetics, coal briquetting and casting
XX sand), as flocculant in soil or coal slurries, as rubber and leather
XX additives, and for production of synthetic polymers, e.g. polyurethane
XX films. Transgenic plants with increased/decreased production of (I)
XX produce starches with altered physical and/or chemical properties such as
XX amylose/amylopectin ratios, degree of branching, mean chain length,
XX phosphate content, gelatinization properties, gel- or film-forming

```

CC properties, or starch grain size or structure. This sequence represents  
CC the soluble starch synthase isolated from wheat (Triticum aestivum L. cv.  
CC Florida).  
XX SQ Sequence 756 AA;  
Query Match 37.7%; Score 862; DB 21: Length 756;  
Best Local Similarity 43.1%; Pred. No. 3.8e-69;  
Matches 194; Conservative 71; Mismatches 147; Indels 38; Gaps 12;  
QY 4 IVMTAAEVAPSKTGGDVTGGPLIELVKGHRVMTIAPRY-----DOYADAWDSVW 57  
Db 141 IVFTGEAAPYAKGGGLDVCGLPITALAARGHVRVWVMPRYLNGSSDKNTAKALYAKH 200  
QY 58 VDIM---GEKRVYFHSIKKGVRWIDHPWFLAKVKGKTSKLYGPRSGADYLDNKKRF 113  
Db 201 IKIPCFGSGSEVTFEYRONVDMVFDHP-----SYHRPGS-LYGDNFGA-FGDNQFRY 253  
QY 114 ALFCKAAIEARVLPFGP---GEDCVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLAI 170  
Db 254 TLLCYAACEAPLILELGGYIYGQNCMFVYNDWHASLVPLLAARYPYGVYRDSRSTLVI 313  
QY 171 HNIAFQGRMEEAFKDKLQAAFDKLAFSQYAKVYTEATPMEEDKPPLTGKTYKIN 230  
Db 314 HNLAHQGVPEASTYDPLGLPPEWYGALEW-----VFPEWARRHALDKG-----EAVN 360  
QY 231 WLKGGITIAADKLVTSFSPNYATEIAAAGGVELDTVI--RAKGGIEGVNMGDIENPKT 288  
Db 361 FLKAVVTADRIIVTSQGYSEWVIT-AEGGQGLNELSSRSKSVLNGVINGIDINDWNP 419  
QY 289 DKFLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFVIGRLEBQKGVDIILALPK 348  
Db 420 DKCLPHYSVDDL-SGKAKCAELQELGLPVREDVPLIGFVIGRLDYQKGLDLIKMAIPE 478  
QY 349 ILATPKVQIAILGTGKAAYEKLVNAIGTKYKRAKGVVVKFSAPLAHMLTAGADEMLVPSR 408  
Db 479 LM-REDVQFVNLGSGDPVIFEGWMRSTESSYKDKFRGWGFSVPVSHRITACGDIILLMPSR 537  
QY 409 FEPGGLIQLHAMHYGTVPVVAAGGLVDV 438  
Db 538 FEPGGLNQLYAMQYGTVPVVGHTGGLRDTV 567

```

RESULT 14

AAW38218
ID AAW38218 standard; Protein; 649 AA.

XX AC AAW38218;

XX DT 22-MAY-1998 (first entry)

XX DE Maize starch synthase type I.

XX KW Maize; starch synthase type I; starch.

XX OS Zea mays.

XX FN DE19619918-A1.

XX PD 20-NOV-1997.

XX PF 17-MAY-1996; 96DE-1019918.

XX PR 17-MAY-1996; 96DE-1019918.

XX PA (PLAN-) PLANITEC BIOTECHNOLOGIE GMBH.

XX PI Froberg C, Kossmann J;

XX DR WPI; 1998-000821/01.

XX DR N-PSDB; AAT95785.

XX PT DNA encoding maize starch synthase type I protein - for producing

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:47:01 ; Search time 11.3212 Seconds
(without alignments)
3719.278 Million cell updates/sec

Title: US-09-980-771A-7

Perfect score: 2288
Sequence: 1 ALDIVMVAEVPWSKTGGL.....AMHYGTVPVASTGGLVDTV 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1301	56.9	608	2 S43341	starch synthase (E
2	1275	55.7	607	1 YUPOY	starch synthase (E
3	1258	55.0	603	2 S61504	glycogen(starch) s
4	1246	54.5	608	2 T10906	starch synthase (E
5	1242	54.3	610	2 F86453	granule-bound star
6	1232.5	53.9	603	1 YUBHY	glycogen(starch) s
7	1230	53.8	609	2 J00703	glycogen(starch) s
8	1229	53.7	609	2 S11481	glycogen(starch) s
9	1204	52.6	615	1 YUWY	glycogen(starch) s
10	1187	51.9	608	2 T14731	glycogen(starch) s
11	1185	51.8	605	1 S07314	glycogen(starch) s
12	870.5	38.0	641	2 T07668	starch synthase (E
13	870	38.0	626	2 J02322	starch synthase (E
14	859	37.5	622	2 T01414	starch synthase (E
15	850	37.2	610	2 T06280	probable starch sy
16	833	36.4	752	2 S61505	glycogen(starch) s
17	822	35.9	732	2 T01208	starch synthase (E
18	815	35.6	491	2 T06798	probable starch sy
19	810	35.4	698	2 T01209	starch synthase (E
20	805.5	35.2	788	2 T07667	glycogen(starch) s
21	660.5	28.9	477	2 B95130	glycogen(starch) s
22	659.5	28.8	477	2 H98000	starch synthase (E
23	628	27.4	484	2 S40051	starch synthase (E
24	623.5	27.3	480	2 H98228	glycogen synthase
25	623.5	27.3	480	2 AF3057	glycogen synthase
26	611	26.7	486	2 H72321	glycogen synthase
27	601	26.3	477	2 A97176	glycogen synthase
28	601	26.3	483	2 C86712	starch synthase (E
29	589	25.7	484	2 F82165	glycogen synthase

30 581 25.4 476 2 AE0479 starch synthase (E
31 578.5 25.3 476 2 E83785 starch (bacterial
32 570.5 24.9 486 2 C96018 probable starch sy
33 566 24.7 477 2 A10995 starch synthase (E
34 565 24.7 477 1 SYEGGL starch synthase (E
35 565 24.7 477 2 B98163 glycogen synthase
36 565 24.7 477 2 C86009 glycogen synthase
37 541 23.6 530 2 AH3194 soluble starch syn
38 528 23.1 1230 2 T07663 starch synthase (E
39 524 22.9 476 2 C64119 glycogen synthase
40 522.5 22.8 463 2 C70363 glycogen synthase
41 520.5 22.7 472 2 A12040 glycogen synthase
42 520 22.7 1025 2 H86250 hypothetical prote
43 506.5 22.1 477 2 S76496 hypothetical prote
44 502 21.9 492 2 AG1810 glycogen (starch)
45 500.5 21.9 1071 2 T04926 starch synthase ho

ALIGNMENTS

RESULT 1

S43341
starch synthase (EC 2.4.1.21) precursor - cassava
N:Alternate names: bacterial-glycogen synthase; glycogen synthase; starch synthase
C:Species: Manihot esculenta (cassava)
C:Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2002
C:Accession: S43341
R:Salehuzzaman, S.N.I.M.; Jacobsen, E.; Visser, R.G.F.
Plant Mol. Biol. 23, 947-962, 1993

A:Title: Isolation and characterization of a cDNA encoding granule-bound starch synthase
A:Reference number: S43341; MUID:94083565; PMID:8260633
A:Accession: S43341
A:Molecule type: mRNA
A:Residues: 1-608 <SAL>

A:Cross-references: EMBL:X74160; NID:g437041; PIDN:CAA52273.1; PID:g437042
C:Genetics:
A:Gene: GBSS; waxy

A:Genome: nuclear

C:Function:

A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose produc

C:Superfamily: starch synthase

C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltra
F:1-78/Domain: transit peptide (amyloplast) #status predicted <TNP>

F:79-608/Product: ADPglucose-starch glucosyltransferase #status predicted <MAT>

Query Match 56.9%: Score 1301; DB 2; Length 608;
Best Local Similarity 57.5%: Pred.No.3.7e-85;
Matches 258; Conservative 51; Mismatches 110; Indels 30; Gaps 7;

QY 2 LDIVMVAEVPWSKTGGLDVTGGTGLIELVKKRHRVMTIAPRYDQYADAWDTSVVVDI- 60

DB 82 MNLIPVGAEGVGPWSKTGGLDVLGGLPPAMAARGHRVMTIVSPRYDQYKDAWDTSVSVELK 141

QY 61 MG---EKVYFHSIKKGVHRVMDHPFLAKVWGTGSKLYGPRSGADYLDNKKRALFC 117

DB 142 IGDRIETVRFHSHYKRGVDRVDFHMFLEKFWGKTGSKIYGPAGLDYQDNQLRFSLLC 201

QY 118 KAAIEAARVLPF-----GP-GEQVFNVDHSHALVPLVKLDEYQPKQFTKAKSVLA 169

DB 202 LAALAPRVNLNSSKNFSGPYGEEVAFANDHALLPCYLKAIQYMGIIYKHAKVAPC 261

QY 170 IHNIAFGQRMEEAFKDTKLQAAFDKLAFLSDGYAKVYTEATPMEEDEKPPITGTYKKI 229

DB 262 LHNIAFGQREAFSDPRLNLPDKFKSSDFDIDGIEK-----PVKG---RKI 304

QY 230 NWLKGIIAALKLVTSVSNYATEIAADAAGGVELDTVIRAKGIEGVNGMDIEWNPKTD 289

DB 305 NWMKAGILESRLVTSVPPYQAQEVLSGVERGVDFNFRKTGTGIAGIINGMDVQWNPVTD 364

QY 290 KFLSAPYQNSVYAGKAAKAAKALQALGELGIPVDPTAPLAFIGRLSEQKGVDIILALPKI 349

DB 365 KYIDHYDATTVMQAKPRLKALQAEVGLPVDNRNPLIGFGRLEQKGSIFVAAISQ- 423

Db 417 AK-FADENVQIVVLGTGKKIMEKQIEVLEEKYPGKAIGITKFNPSLAHKLIIAGADFIIVP 475
 QY 407 SRFEPCGLIOLHAMHYGVVAVSTGGLVDIV 438
 Db 476 SRFEPCGLVQLHAMPIGIVPIVSSGTGLVDIV 507

RESULT 4

T10906
 starch synthase (EC 2.4.1.21) - sweet potato
 N:Alternate names: starch synthase
 C:Species: Ipomoea batatas (sweet potato)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002
 C:Accession: T10906

R:Wang, S.J.; Yeh, K.W.; Tsai, C.Y.
 submitted to the EMBL Data Library, December 1995
 A:Accession: T10906
 A:Reference number: Z17212
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-608 <W>
 A:Cross-references: EMBL:U44126; NID:g1172158; PID:g1172159
 A:Experimental source: cv. Tainong; tuberous root
 C:Genetics: SS67
 C:Gene: SS67
 C:Function:
 A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPGlucose producing a
 A:Pathway: starch biosynthesis
 C:Superfamily: starch synthase
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 54.5%; Score 1246; DB 2; Length 608;
 Best Local Similarity 56.3%; Pred. No. 3.2e-81;
 Matches 253; Conservative 48; Mismatches 118; Indels 30; Gaps 7;

QY 2 LDIVMAAEVAPWSKTGGLGVDVTGGLPIELVKKRHRVMTIAPRYDOYADAWDTVVVVDI- 60
 Db 82 MNLVFGCEGEPWCKTGGLGVDVGLPLPALAARGHRVMTICPRYDOYKDAWETCVVVEQ 141
 QY 61 MG---EKVYRPHSHKGGVHRVWIDHPWFLAKVWGKTGSKLYGPRGADYLDNHRKRALFC 117
 Db 142 VGDRIEPRVRFPHSKYKRGVDFVDFHPELEKVGWKTGSMLYGPRAGKDYKDNQLRFLSLC 201
 QY 118 KAAIEAARVLPF-----GP-GEDEVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA 169
 Db 202 QAALAEAPVNLNLSKYSFGPYGEDVVFVANDWHTALLPCYIKMYQSRGIYMNKAVAF 261
 QY 170 IHNIAFOGRMWEAFKDTKLPAQAFDKLAFSDGAKVYTEATPMEDEKPPITGKTKYKI 229
 Db 262 IHNIAOGRFAFSDFLNLNLPDEYKGSFDFIDGYDK-----PVKG---RKI 304
 QY 230 NNLKAGGIIAADKLVTSPNYATEAADAAGVGLDVTIRAKGIGIVNGMDIEWNP 289
 Db 305 NNMKAGIREADRVFTVSPNYAKELVSCVSKGVLDNHRDGCITGICNGMDTQEWNPATD 364
 QY 290 KFLSAPYDONSVAAGKAAKALQAEGLPLVDPTAPLFAFVIGRLEEKGVDIILAAALPKI 349
 Db 365 KYLAVKDIITVYMAQKPLKALQAVGLPVDRIPLIGFVIGRLEEKQKGSIDILAAATSKF 424
 QY 350 LATPKVQIAILGTGKAAEYKILVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVPSRF 409
 Db 425 ISM-DVQIILGTCKKFEQIQELEVNYDPKARGVAKFNYPVLAHMITAGADFMVPSRF 483
 QY 410 EPCGLIOLHAMHYGVVAVSTGGLVDIV 438
 Db 484 EPCGLIOLHAMRYGTPICASTGGLVDIV 512

RESULT 5

F86453
 granule-bound starch synthase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: F86453
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alor
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzla
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F86453
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-610 <STO>
 A:Cross-references: GB:AE005172; NID:96910568; PID:AAF31273.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1
 C:Superfamily: starch synthase

Query Match 54.3%; Score 1242; DB 2; Length 610;
 Best Local Similarity 55.3%; Pred. No. 6.1e-81;
 Matches 250; Conservative 59; Mismatches 107; Indels 36; Gaps 9;

QY 2 LDIVMAAEVAPWSKTGGLGVDVTGGLPIELVKKRHRVMTIAPRYDOYADAWDTVVVVDI- 60
 Db 84 MSVIFGAEGVSPWSTGGLGVDVGLPLPALAARGHRVMTICPRYDOYKDAWETCVVQIK 143
 QY 61 MCEK---VRYPHSHKGGVHRVWIDHPWFLAKVWGKTGSKLYGPRGADYLDNHRKRALFC 117
 Db 144 VGDKVENVRFFHCYKRGVDFVDFHPIFLAKVWGKTGSKYIYGPITGVNDNQLRFLSLC 203
 QY 118 KAAIEAARVLPF-----GP-GEDEVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA 169
 Db 204 QAALAEAPVNLNLSKYSFGPYGEDVVFVANDWHTALLPCYIKMYQSRGIYMNKAVAF 263
 QY 170 IHNIAFOGRMWEAFKDTKLPAQAFDKLAFSDGAKVYTEATPMEDEKPPITGKTKYKI 226
 Db 264 IHNIAOGRFAFDDYSLNLNLPISFKSFD---FMDGYE-----PVKG--- 303
 QY 227 KKNLKGIIAADKLVTSPNYATEAADAAGVGLDVTIRAKGIGIVNGMDIEWNP 286
 Db 304 KKNMKAALIEAHRLVTVSPYTAQELTSGVDRGVELHKLKMKTVSGVINGMDYQEWNP 363
 QY 287 KTDKFLSAPYDONSVAAGKAAKALQAEGLPLVDPTAPLFAFVIGRLEEKGVDIILAAAL 346
 Db 364 STDKVIDIKYDITVTDAKPLKALQAVGLPVDRIPLIGFVIGRLEEKQKGSIDILVEAI 423
 QY 347 PKLATPKVQIAILGTGKAAEYKILVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMVLP 406
 Db 424 SKFMGL-NVQVILGTGKKKEAQILEEEKPFGKAVGKPNVLAHMITAGADFIIVP 482
 QY 407 SRFEPCGLIOLHAMHYGVVAVSTGGLVDIV 438
 Db 483 SRFEPCGLIOLHAMRYGTPIVAVSTGGLVDIV 514

RESULT 6

YUBHY
 glycogen(starch) synthase (EC 2.4.1.11) precursor - barley
 N:Alternate names: starch synthase
 C:Species: Hordeum vulgare (barley)
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 02-Aug-2002
 C:Accession: S01727; S01728
 R:Roche, W.; Becker, D.; Salamini, F.
 Nucleic Acids Res. 16, 7185-7186, 1988
 A:Title: Structural analysis of the waxy locus from Hordeum vulgare.
 A:Reference number: S01727; MUID:88303345; PMID:2970062
 A:Accession: S01727
 A:Molecule type: DNA
 A:Residues: 1-603 <ROI>
 A:Cross-references: EMBL:X07931; NID:q19126; PID:CAA30755.1; PID:g295809

A:Accession: S01728

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-603 <ROH2>

A:Cross-references: EMBL:X07932; NID:gl9128; PIDN:CAA30756.1; PID:gl9129

C:Genetics:

A:Gene: waxy

A:Introns: 106/3; 133/3; 166/3; 218/1; 251/3; 369/3; 429/3; 493/3; 522/3; 565/3

C:Function:

A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose producing

A:Pathway: starch biosynthesis

C:Superfamily: starch synthase

C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltrans

F:1-72/Domain: transit peptide (amyloplast) #status predicted <NP>

F:73-603/Product: UDPglucose-starch glycosyltransferase #status predicted <MA>

Query Match 53.9%; Score 1232.5; DB 1; Length 603;

Best Local Similarity 54.1%; Pred. No. 2.9e-80;

Matches 243; Conservative 60; Mismatches 117; Indels 29; Gaps 6;

QY 2 LDIWVAEAPVPSKSTGGGLGVTGGLPIELVKRGHVRMTIAPRYDQYADAMDTSVVVDIM 61

Db 76 MNLVFGAEMAPNSKTGGGLGVLGPPAMAANGHRVWVSPRYDQYKDAWDTSVISEIK 135

QY 62 ----GEKRVFHSIKKGVRHWIDHPWFLAKVWGTGSKLYGPRSGADYLDNHRKRALFC 117

Db 136 VADEYERVRFFHCYKRGVDRVFDHPWFLKVRGKTREKIYGPDAGTDEYDQQRFSLLC 195

QY 118 KAAEAARVL-----GP-GEDEVFVANDWHSALVPLLLKDEYOPKGOFTKAKSVLA 169

Db 196 QAALEAPRILNINNPFSGYGEDVFCVNDWHTGLACVLSYNSGIRYAKVAFC 255

QY 170 IHNIAFGRMWEEAFKDTKLPPQAAFDKLAISDGAKVYVTEATPMEDEKPLTGTGYKKI 229

Db 256 IHNISYQGRSFDFDAQNLDPKFSFDFIDGYK-----PVEG---RKI 298

QY 230 NNLKGIIADKLVTSFNATETADAAGGVELDTVIRAKGIEGIVNGMDIEWNPKTD 289

Db 299 NNMKAGILQADKLVTSFNYAEELISGEARCELDNIMRLTGITGIVNGMDVSEWDPTKD 358

QY 290 KFLSAPYDONSIVYAGKAAKALQALGELPVDPTAPLFAFGRLEEQKGVDIILAAALPKI 349

Db 359 KFLAVNDYITTALEAKALNKEALQAEGLPVDKRVPLVAFGRLEEQKGPDMVMAAIEPI 418

QY 350 LATPKVQITAILGTGKAAYEKLIVNAIGTKYGRKAGVVKFSAPLAHMLTAGADEMLVPGRF 409

Db 419 LKEEDVQIILLGTCKKFEKLLKSMEEKYPGKRVAVRFPNAPLAHQMMAGADLLAVTSRF 478

QY 410 EPCGLIQLHAMHYGTVPVASTGGGLVDIV 438

Db 479 EPCGLIQLQGMRYGTGTCVCASTGGGLVDIV 507

RESULT 7

QJ00703

glycogen(starch) synthase (EC 2.4.1.11) - rice

N:Alternate names: granule-bound starch synthase

C:Species: Oryza sativa (rice)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-2002

C:Accession: JQ0703

R:Wang, Z.Y.; Wu, Z.L.; Xing, Y.Y.; Zheng, F.G.; Guo, X.L.; Zhang, W.G.; Hong, M.M.

Nucleic Acids Res. 18, 5898, 1990

A:Title: Nucleotide sequence of rice waxy gene.

A:Reference number: JQ0703; MUID:91016948; PMID:2216792

A:Accession: JQ0703

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-609 <WAX>

A:Cross-references: EMBL:X53694

A:Experimental source: strain subsp. japonica Hengfeng

C:Genetics:

A:Gene: waxy

A:Introns: 114/1; 141/1; 174/1; 204/1; 225/2; 259/1; 295/3; 377/1; 436/1; 500/1; 529/1;

C:Function:

A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose produc

C:Superfamily: starch synthase

C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltr

Query Match 53.8%; Score 1230; DB 2; Length 609;

Best Local Similarity 53.7%; Pred. No. 4.4e-80;

Matches 241; Conservative 62; Mismatches 116; Indels 30; Gaps 6;

QY 2 LDIWVAEAPVPSKSTGGGLGVTGGLPIELVKRGHVRMTIAPRYDQYADAMDTSVVVDI- 60

Db 83 MNLVFGAEMAPNSKTGGGLGVLGPPAMAANGHRVWVSPRYDQYKDAWDTSVVAEVK 142

QY 61 ---MGEKRVFHSIKKGVRHWIDHPWFLAKVWGTGSKLYGPRSGADYLDNHRKRALFC 117

Db 143 VADRYERVRFFHCYKRGVDRVFDHPSPLEKVGWGTGKIYGPDTGVDYKDNQMRFSLLC 202

QY 118 KAAEAARVL-----PQCP---GECVFNANDWHSALVPLLLKDEYOPKGOFTKAKSVLA 169

Db 203 QAALEAPRILNINNPFYKGYGEDVFCVNDWHTGLASYLKNNYPNGIYRNKVAFC 262

QY 170 IHNIAFGRMWEEAFKDTKLPPQAAFDKLAISDGAKVYVTEATPMEDEKPLTGTGYKKI 229

Db 263 IHNISYQGRFAFEDYPENLSERFSFDFIDGY-----DTPVEG-----RKI 305

QY 230 NNLKGIIADKLVTSFNATETADAAGGVELDTVIRAKGIEGIVNGMDIEWNPKTD 289

Db 306 NNMKAGILEADRVLTSPYAEELTSGIARGCELDNIMRLTGITGIVNGMDVSEWDPSKD 365

QY 290 KFLSAPYDONSIVYAGKAAKALQALGELPVDPTAPLFAFGRLEEQKGVDIILAAALPKI 349

Db 366 KIITAKYDATTAEAKALNKEALQAEGLPVDKRVPLIATFGRLEEQKGPDMVMAAIEPEL 425

QY 350 LATPKVQITAILGTGKAAYEKLIVNAIGTKYGRKAGVVKFSAPLAHMLTAGADEMLVPGRF 409

Db 426 M-QEDVQIVLLGTCKKFEKLLKSMEEKYPGKRVAVRFPNAPLAHMLTAGADVLAVPSRF 484

QY 410 EPCGLIQLHAMHYGTVPVASTGGGLVDIV 438

Db 485 EPCGLIQLQGMRYGTACACASTGGGLVDIV 513

RESULT 8

S11481

glycogen(starch) synthase (EC 2.4.1.11) precursor - rice

N:Alternate names: starch synthase; waxy protein

C:Species: Oryza sativa (rice)

C:Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2002

C:Accession: S11481; S22519; S30485; PC2190; JQ2224

R:Wang, Z.Y.; Wu, Z.L.; Xing, Y.Y.; Zheng, F.G.; Guo, X.L.; Zhang, W.G.; Hong, M.M.

Nucleic Acids Res. 18, 5898, 1990

A:Title: Nucleotide sequence of rice waxy gene.

A:Reference number: JQ0703; MUID:91016948; PMID:2216792

A:Accession: S11481

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-609 <WAX>

A:Cross-references: EMBL:X53694; NID:9577598; PIDN:CAA37732.1; PID:9577599

R:Okagaki, R.J.

Plant Mol. Biol. 19, 513-516, 1992

A:Title: Nucleotide sequence of a long cDNA from the rice waxy gene.

A:Reference number: S22519; MUID:92322986; PMID:1377969

A:Accession: S22519

A:Molecule type: mRNA

A:Residues: 1-609 <OKA>

A:Cross-references: EMBL:X62134; NID:g20402; PIDN:CAA44065.1; PID:g20403

R:Hitano, H.Y.; Sano, Y.

Plant Cell Physiol. 32, 989-997, 1991

A:Title: Molecular characterization of the waxy locus of rice (Oryza sativa).

A:Reference number: S30485

A:Accession: S30485

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-609 <HIR>
A:Cross-references: EMBL:X58228; NID:g20400; PIDN:CAA1186.1; PID:g20401
A:Accession: PC2190
A:Molecule type: protein
A:Residues: 78-113 <H12>
A:Experimental source: leaf, cDNA POSLHC2120
C:Comment: This protein is involved in amylose synthesis in the rice endosperm.
C:Genetics:
A:Gene: waxy
A:Introns: 113/3; 140/3; 173/3; 203/3; 225/1; 258/3; 295/2; 376/3; 435/3; 499/3; 528/3;
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose producing
A:Pathway: starch biosynthesis
C:Superfamily: starch synthase
C:Keywords: amyloplast; chloroplast; glycogen/starch biosynthesis; glycosyltransferase;
F:1-77/Domain: transit peptide (amyloplast) #status predicted <INP>
F:78-609/Product: glycogen (starch) synthase #status experimental <MAT>

Query Match 53.7%; Score 1229; DB 2; Length 609;
Best Local Similarity 53.9%; Pred. No. 5,2e-80;
Matches 242; Conservative 61; Mismatches 116; Indels 30; Gaps 6;

QY 2 LDIVVAAEVPWSTKGTGLGVDVGGTGLPIELVYKRGHRVMTIAPRYDQYADADMTSVVVDI- 60
DB 83 MNVVFVGAEMAPWSTKGTGLGVDVGGTGLPAPMAAANGHRVWVISPRIYDQYKDAWDTSVVAEIK 142
QY 61 ---MGEKRYRPHSIKKGVRHWIDHPWFLAKVWGTGSKLYGPRSGADYLDNKKRFALEFC 117
DB 143 VADRYERVRFHCYKRGVDRVFDHPSELEKVGWTKGKIYGPDTGVYKDNQMRFSLLC 202
QY 118 KAAIEAARVL-----PFGP-----GEDCVFVANDWHSALVPVLLKDEYQPKGTFKAKSVIA 169
DB 203 QAALAEAPRLNNPFGKTYGDEGVFVPCNDWHTGGLASLYKNQYNGIYRNKAVAF 262
QY 170 IHNIAFOGRMWEAFKDTKLPOAAFDKLAISDGYAKVYTEATPMEDEKPLTGKTYKKI 229
DB 263 IHNISYGRFAFEDYPELNLSEFRSSFDIDGY-----DTPVEG-----RKI 305
QY 230 NWLKGIIAADKLVTSVPNYATEATAADAGVVELDVTIRAKGIGIVNGMDEWNPRTD 289
DB 306 NWMKAGILEADRVLTSPYAEELISGTARGCELDNIMRLGITGIVNGMDVSEWDPSKD 365
QY 290 KELSAPYDQNSVYAGKAAKALQALQELGLPVDPPTAPFAFTGRLEEOOGVDIILAALEPKI 349
DB 366 KYITAKDYATTAIAKALNKALQALQELGLPVDRKPLIAFTIGRLEEOOGVDVMAAIDEL 425
QY 350 LATPKVQIAIIGTGAAYEKVLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADEMLVPSRF 409
DB 426 M-QEDVQVILVLTGKTKKFEKLLKSMEEKYPCGVRAVVKFNAPLAHMLMAGADVLAVPSRF 484
QY 410 EPCGLIOLHAMHYGTVPVWASTGGLVDTV 438
DB 485 EPCGLIOLQGMRYGTGTPCACASTGGLVDTV 513

RESULT 9
YUWY
glycogen(starch) synthase (EC 2.4.1.11) precursor - wheat
N:Alternate names: starch synthase
C:Species: Triticum aestivum (common wheat)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 02-Aug-2002
C:Accession: S16261; S33636
R:Clark, J.R.; Robertson, M.; Ainsworth, C.C.
Plant Mol. Biol. 16, 1099-1101, 1991
A:Title: Nucleotide sequence of a wheat (Triticum aestivum L.) cDNA clone encoding the
A:Reference number: S16261; MUID:91322506; PMID:1863765
A:Accession: S16261
A:Molecule type: mRNA
A:Residues: 1-615 <CLA>
A:Cross-references: EMBL:X57233; NID:g21901; PIDN:CAA0509.1; PID:g21902
R:Ainsworth, C.; Clark, J.; Baisdon, J.
Plant Mol. Biol. 22, 67-82, 1993
A:Title: Expression, organisation and structure of the genes encoding the waxy protein

A:Reference number: S33636; MUID:93271462; PMID:8499619
A:Accession: S33636
A:Molecule type: protein
A:Residues: 71-75, 'X', 77-78 <AIN>
C:Genetics:
A:Gene: waxy
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose produc
A:Pathway: starch biosynthesis
C:Superfamily: starch synthase
C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltra
F:1-70/Domain: transit peptide (amyloplast) #status predicted <TN>
F:71-615/Product: UDPglucose-starch glycosyltransferase #status experimental <MAT>

Query Match 52.6%; Score 1204; DB 1; Length 615;
Best Local Similarity 51.7%; Pred. No. 3,2e-78;
Matches 238; Conservative 60; Mismatches 122; Indels 40; Gaps 5;

QY 2 LDIVVAAEVPWSTKGTGLGVDVGGTGLPIELVYKRGHRVMTIAPRYDQYADADMTSVVVDI- 60
DB 77 MNVVFVGAEMAPWSTKGTGLGVDVGGTGLPAPMAAANGHRVWVISPRIYDQYKDAWDTSVISEIK 136
QY 61 ---MGEKRYRPHSIKKGVRHWIDHPWFLAKVWGTGSKLYGPRSGADYLDNKKRFALEFC 117
DB 137 VADRYERVRFHCYKRGVDRVFDHPSELEKVGWTKGKIYGPDTGVYKDNQMRFSLLC 196
QY 118 KAAIEAARVLPP-----GP-----GEDCVFVANDWHSALVPVLLKDEYQPK 158
DB 197 QAALAEVPRILNNPFGSPVAMLCRAVPRAGEDVVFVPCNDWHTGGLACLYKSNYQSN 256
QY 159 GQFTKAKSVLAHNIAFOGRMWEAFKDTKLPOAAFDKLAISDGYAKVYTEATPMEDEK 218
DB 257 GIYRTAKVAFCHNLSYQGRFSFDDFAQLNLPDREKSSFDIDGYDK----- 303
QY 219 PELTGKTKYKINWLAGGIITADKLVTSVPNYATEATAADAGVVELDVTIRAKGIGIVNG 278
DB 304 -PVEG---RKINWMAKAGILQADKLVTSVPYAEELISGEARCELDNIMRLGITGIVNG 359
QY 279 MDIEWNPRTDKLSAPYDQNSVYAGKAAKALQALQELGLPVDPPTAPFAFTGRLEEOOG 338
DB 360 MDVSEWDIPDKFPLVNDVTTALGKALNKALQALQELGLPVDRKPLVIAFTIGRLEEOOG 419
QY 339 VDIILAALEPKIATPKVQIAIIGTGAAYEKVLVNAIGTKYKGRAGVVKFSAPLAHMLTA 398
DB 420 PDVMAIATPEIVKEDVQVILVLTGKTKKFEKLLKSMEEKYPCGVRAVVKFNAPLAHOMA 479
QY 399 GADFMVPSRPEPCGLIOLHAMHYGTVPVWASTGGLVDTV 438
DB 480 GADVLAVTSRPEPCGLIOLQGMRYGTGTPCACASTGGLVDTV 519

RESULT 10
TI4731
glycogen(starch) synthase (EC 2.4.1.11) precursor, granule-bound - sorghum
N:Alternate names: starch synthase, granule-bound
C:Species: Sorghum bicolor (sorghum)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002
C:Accession: TI4731
R:Hsing, Y.C.
submitted to the EMBL Data Library, April 1995
A:Reference number: Z181173
A:Accession: TI4731
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-608 <HST>
A:Cross-references: EMBL:U23945; NID:gl255713; PID:gl255714
A:Experimental source: strain I2311; young seed
C:Genetics:
A:Genome: nuclear
A:Note: Wx
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose produc
A:Pathway: starch biosynthesis

C:Superfamily: starch synthase
C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase;
F;1-77/Domain: transit peptide (amyloplast) #status predicted <TNP>
F;78-608/Product: UDPglucose-starch glucosyltransferase #status predicted <MAT>

Query Match 51.9%; Score 1187; DB 2; Length 608;
Best Local Similarity 52.6%; Pred. No. 5.2e-77;
Matches 236; Conservative 63; Mismatches 120; Indels 30; Gaps 8;

QY 2 LDIVMVAEAVPWSKTGGGLDGTGGLPIELVLRKGRHVMITAPRYDQYADAWDTISVVVDI- 60
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
82 MNVVFVGAEMAPWSKTGGGLDVLGGLPPAMAANGHRVMVSPRYDQYKDAWDTISVVSEIK 141
QY 61 MG---EKVYFHSIKGVHRWIDHPWFLAKVWGKTGSKLYGPSGADYLDNKHKRALFC 117
Db ||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
142 MGDGYETVRFFHCYRKGVRDVFDHPLFLERVWGKTEKIYGPDACTDYKDQLRFSLLC 201
QY 118 KAAIEARVL-----PF--GP--GEDCVFVANDWHSALEVPVLLKDEYQPGQTAKSVLA 169
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
202 QAALEAPRIULNNPNFYSGPYGVEDVVCNDWHTGPLSCYLKSNYQSNGIYKDKATAFC 261
QY 170 IHNIAPQGRWEAEAFKDTKLPOAEPDKLAFSDGYAKVIYEAATPEMEDEKPPLTGTYKKI 229
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
262 IHNISYQGFAFSDFPELNLPERFKSFFIDIGYEK-----PVEG----RKI 304
QY 230 NMLKGGITIAADLVTVSPNVAYTAADAAGGVVELDPVIRAKGTGEGVINGMDIEENPKTD 289
Db ||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
305 NNWKAGILEADRVLTVSPYYAEELISSIARGCELDNIMRLTGITGVINGMDVSEWDPSKD 364
QY 290 KFLSYPDONSIVYAGKAALKEALQAEGLPVDPFTAPLFAPIGHLEQKGVDDIIILALPKI 349
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
365 KYTAVKYDVSTAVEAKLNKEALQAEVGLPVDRKIPLVAFIGRLEEQKGPDMVMAAI-P-L 423
QY 350 LAPPKVOIALTLGGKAAYPEKLVNAICTGKGRAGVVKTSAPLAHMLTAGPDMLVPSRF 409
Db ||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
424 LMEDIQIVLLGCCKKKFERMLMSAEKYPDKVRAVVKFNAAALAHMAGDLLAVTSRF 483
QY 410 EPGCLLIOLHAMHYGVTPVVAAGTGLVDVT 438
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
484 EPGCLILOGMRYGTGPCACASTGGLVDTI 512

RESULT 11
S07314
glycogen(starch) synthase (EC 2.4.1.11) precursor - maize
N;Alternate names: starch synthase; UDP-glucose starch glycosyltransferase, starch granule
C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 02-Aug-2002
C;Accession: S07314
R;Kloesgen, R.B.; Gierl, A.; Schwarz-Sommer, Z.; Saedler, H.
Mol. Gen. Genet. 203, 237-244, 1986
A;Title: Molecular analysis of the waxy locus of Zea mays.
A;Reference number: S07314
A;Accession: S07314
A:Molecule type: DNA
A:Residues: 1-605 <KIO>
A:Cross-references: EMBL:X03935; NID:g22509; PIDN:CAA27574.1; PID:g1644339
A:Experimental source: line C
A>Note: translation of the nucleotide sequence is not complete
A>Note: part of this sequence, including the amino end of the mature protein, was confirmed by sequencing
C;Genetics:
A:Gene: waxy
A:Introns: 107/3; 134/3; 167/3; 197/3; 219/1; 252/3; 289/2; 370/3; 431/3; 495/3; 524/3;
C;Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose producing glucose-1-phosphate
C;Superfamily: starch synthase
C;Keywords: amyloplast; chloroplast; glycogen/starch biosynthesis; glycosyltransferase;
F;1-72/Domain: transit peptide (amyloplast) #status predicted <TNP>
F;73-605/Product: glycogen (starch) synthase #status experimental <MAT>

Query Match 51.8%; Score 1185; DB 1; Length 605;
Best Local Similarity 52.0%; Pred. No. 7.1e-77;
Matches 234; Conservative 67; Mismatches 119; Indels 30; Gaps 8;

```

Qy 289 DKFLSAPYDQNSVYAGKAAAEALQELGVPDTPAPLEAFIGRLBEQKGVDIILAALPK 348
Db 414 DKFLPYHVSDDL-SGKAKCAELQELGLPVRPDPFLGIFGRLDYQKGIIDIKLAIPD 472
Qy 349 ILATPKVQIILGTGKAAYEKIVNAIGTKYGRKAGVVKFSAPLAHMLTAGADFMVLVPSR 408
Db 473 LM-RDNIQFVMLGSDPGFEGHWRSTESYRDKFRGWGVSFVPSRITAGCDILLMPSR 531
Qy 409 FEPGCLQLHAMHYCTVPVVASTGGGLVDTV 438
Db 532 FEPGCLNOLYAMQYGTVPVWHGTGGLRDTV 561

RESULT 14
T01414
starch synthase (EC 2.4.1.21) precursor - maize
N:Alternate names: starch synthase I
C:Species: Zea mays (maize)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Aug-2002
R:Accession: T01414
R:Knight, M.E.; Harn, C.; Lilley, C.E.R.; Guan, H.P.; Singletary, G.W.; Mu-Por-
plant J. 14, 613-622, 1998
A:Title: Molecular cloning of starch synthase I from maize (W64A) endosperm an-
A:Reference number: 214279; MUID:98340555; PMID:9675904
A:Accession: T01414
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-622 <KNT>
A:Cross-references: EMBL:AF036891; NID:G2828011; PIDN:AAB99957.1; PID:G2828012
A:Experimental source: strain W64A; endosperm
C:Genetics:
A:Gene: Ssl
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose p-
A:Superfamily: starch synthase
C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase;

```

Query Match	37.5%	Score 859;	DB 2;	Length 622;
Best Local Similarity	42.2%;	Pred. N0.1.4e-53;		
Matches	190;	Conservative 77;	Mismatches 145;	Indels 38;
Gaps	12			
QY	4	IVMVAARVAPMSKGTGLGDVTGGPIELVAKGHRVMTAPRY-----DOYADADWTSV	57	
Db	134	IVFTGASPYAKSGGLGDCVGLPVALAARGHRVVMVPRYLNGTSOKNYANAFYTERK	193	
QY	58	VDIM--GE-KVRYPFHSIKKGVRHWIDHPFLAKVWGKTSGLSGSPGADYLDNHKRF	113	
Db	194	IRIPCFGGEHEVTFEHEYRDSVDWVVFDPSPV-----HRPGNLVYDKDFGA-FGDNQFRY	246	
QY	114	ALFCKAAIEAARVLPPFGP--GECQVFVANDWHSALVPVLLKDEYQPKQGFKAKSVAL	170	
Db	247	TLLCYACEAPLILIELGYYIQNCMFVNDWHSALVPVLLAARVYGVYKDSRLVY	306	
QY	171	HNIAFGRMWEEAPKDTKLPOAADFKLAFSDGYAKVYTEATPMEEDKPLPLTKGYKKIN	230	
Db	307	HNLAHQVEPASTYPDGLPEWYGALEW-----VFPEWARRHALDKG-----EAVN	353	
QY	231	WLKGGIITADKLVTPSNYATFIAADAGGVELDTVI--RAGTIEGVNGMDIEWNPKT	288	
Db	354	FLKAVVTADRIVTYSGYSEWVT-ABGGGGLNELLSSRKSVLNGVINGVIDINDWNPAT	412	
QY	289	DKFLSAPYDQNSVYAGKAAKEALQAEILGLVPDPTAPLFAFAGRLKEOGKQDIIILAALEPK	348	
Db	413	DKCIPCHYSVDLL-SGKAKCKGALQKELGLPIRPDVPPLIGFIGRLDYQKGDILQILIPD	471	
QY	349	ILATPKVQIAILGTGKAAYEKLVAIGTKYGRAGVVKFSAPLAHMTAGADFMVPSR	408	
Db	472	LM-REDQVFMVLGSDPELEDNMWKESTESIFKDKFRGWWGVFSVPVSHRIITAGCDIILMPSR	530	
QY	409	FEPCLGTLHAMHYGTVPVVASTGGLVDVT	438	
Db	531	FEPCCGLNOLYAMCYGTVPVVAHTSGI RDVT	560	

search completed: June 4, 2003, 14:37:30
Job time : 16.3212 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 13:50:41 ; Search time 5.88117 Seconds
(without alignments)
3088.950 Million cell updates/sec

Title: US-09-980-771a-7

Perfect score: 2288

Sequence: 1 ALDIVMAAEVAPWSKTGGL.....AMHYGTVPVVASTGGLVDVTV 438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1301	56.9	608	1	UGST_MANES
2	1277	55.8	608	1	UGST_ANTMA
3	1275	55.7	607	1	UGST_SOLTU
4	1258	55.0	603	1	UGST_PEA
5	1246	54.5	608	1	UGST_IPOBA
6	1232.5	53.9	603	1	UGST_HORVU
7	1229	53.7	609	1	UGST_ORYGL
8	1229	53.7	609	1	UGST_ORYSA
9	1204	52.6	615	1	UGST_WHEAT
10	1187	51.9	608	1	UGST_SORBI
11	1185	51.8	605	1	UGST_MAIZE
12	870.5	38.0	641	1	UGS2_SOLTU
13	870	38.0	626	1	UGS2_ORYSA
14	850	37.2	610	1	UGS2_WHEAT
15	833	36.4	752	1	UGS3_PEA
16	805.5	35.2	788	1	UGS3_SOLTU
17	660.5	28.9	477	1	GLGA_STRPN
18	638.5	27.5	485	1	GLGA_BACST
19	628	27.4	484	1	GLGA_BACSU
20	623.5	27.3	480	1	GLGA_AGR5
21	615	26.9	480	1	GLG1_RHIME
22	611	26.7	486	1	GLGA_THEMA
23	605.5	26.5	480	1	GLGA_RHTR
24	601	26.3	477	1	GLGA_CLOBB
25	601	26.3	478	1	GLGA_LACLA
26	589	25.7	484	1	GLGA_VIBCH
27	587.5	25.7	482	1	GLGA_CLOPE
28	581	25.4	476	1	GLGA_VERPE
29	578.5	25.3	476	1	GLGA_BACHD
30	575.5	25.2	481	1	GLGA_RHILLO
31	570.5	24.9	486	1	GLG2_RHIME
32	566	24.7	477	1	GLGA_SALTI
33	565	24.7	477	1	GLGA_ECOLI

34	559	24.4	477	1	GLGA_SALTY	P05416 salmonella
35	552	24.1	480	1	GLGA_PASMU	Q9c9n1 pasteurella
36	528	23.1	1230	1	UGS4_SOLTU	Q43846 solanum tub
37	527.5	23.1	465	1	GLGA_SYNP7	Q93577 synechococc
38	524	22.9	476	1	GLGA_HAEIN	P45179 haemophilus
39	522.5	22.8	463	1	GLGA_AOUAE	O66935 aquifex aeo
40	520.5	22.7	472	1	GLGA_ANASP	Q8YVU5 anabaena sp
41	514	22.5	477	1	GLGA_RHOSH	Q9RRH6 rhodobacter
42	506.5	22.1	477	1	GLGA_SYNY3	P74521 synechocyst
43	502	21.9	492	1	GLG2_ANASP	Q8Z0G9 anabaena sp
44	496.5	21.7	491	1	GLG2_SYNY3	P76233 synechocyst
45	493.5	21.6	461	1	GLGA_FUSNN	Q8RR65 fusobacteri

ALIGNMENTS

RESULT 1

ID	UGST_MANES	STANDARD;	PRT;	608 AA.
AC	Q43784;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Granule-bound glycogen [starch] synthase, chloroplast precursor			
DE	(EC 2.4.1.11).			
GN	WAXY OR GBSS.			
OS	Manihot esculenta (Cassava) (Manioc).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid 1; Malpighiales; Euphorbiaceae; Manihot.			
OX	NCBI_TaxID=3983;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. M.COI.22; TISSUE=Tuberous root;			
RX	MEDLINE=94083565; PubMed=8260633;			
RA	Salchuzman S.N., Jacobsen E., Visser R.G.F.;			
RT	"Isolation and characterization of a cDNA encoding granule-bound			
RT	starch synthase in cassava (Manihot esculenta Crantz) and its			
RT	antisense expression in potato.";			
RL	Plant Mol. Biol. 23:947-962(1993).			
CC	!- FUNCTION: RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE IN RESERVE			
CC	STARCH.			
CC	!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =			
CC	UDP + {(1,4)-alpha-D-glucosyl}(N+1).			
CC	!- PATHWAY: Starch biosynthesis.			
CC	!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.			
CC	!- TISSUE SPECIFICITY: SYNTHESIZED IN A NUMBER OF DIFFERENT ORGANS,			
CC	BUT MOST ABUNDANTLY IN TUBERS.			
CC	!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE			
CC	FAMILY.			

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR	EMBL; X74160; CAA52273.1; .			
DR	InterPro; IPR001296; Glycos_transf_1.			
DR	Pfam; PF00534; Glycos_transf_1; 1.			
KW	Glycogen biosynthesis; Transferase; glycosyltransferase;			
KW	Transit peptide; Chloroplast; Starch biosynthesis.			
FT	TRANSIT 1 78 CHLOROPLAST (BY SIMILARITY).			
FT	CHAIN 79 608 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.			
FT	BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).			
SQ	SEQUENCE 608 AA; 66968 MW; C9C970CD3011BDD8 CRC64;			

Query Match 56.9%; Score 1301; DB 1; Length 608;
Best Local Similarity 57.5%; Pred. No. 1.3e-85;
Matches 258; Conservative 51; Mismatches 110; Indels 30; Gaps 7;

*Sequence of the structural gene for granule-bound starch synthase of
RT potato (Solanum tuberosum L.) and evidence for a single point
RT deletion in the amf allele. ;
RL Mol. Gen. Genet. 228:240-248(1991).
RN [2]

RP REVISIONS.
RA van der Lei J. F.R.;
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Dongnong 303;
RA Dai W.L., Deng W., Cui M., Xiu M., Zhao S.Y., Wang X.M.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; X58453; CAA41359.1; -;
DR EMBL; X83220; CAA58220.1; -;
DR PIR; S16555; YUPOY.
DR InterPro; IPR001296; Glycos.transf.1.
DR Pfam; PF00534; Glycos.transf.1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Starch biosynthesis.
FT TRANSIT 1 77 CHLOROPLAST.
FT CHAIN 78 607 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 95 95 UDP-GLUCOSE (BY SIMILARITY).
FT CONFLICT 130 130 A -> T (IN REF. 3).
FT CONFLICT 398 398 I -> V (IN REF. 3).
SQ SEQUENCE 607 AA; 66575 MW; 2A377865CEFA650 CRC64;

Query Match 55.7%; Score 1275; DB 1; Length 607;
Best Local Similarity 56.3%; Pred. No. 9.6e-84;
Matches 253; Conservative 54; Mismatches 112; Indels 30; Gaps 7;
QY 2 LDIVVAAEVPWSKTGGLGVDVTGGPLTELKVRHVRMTIAPRYDQYADAWDTSVVVDI- 60
DB 81 MNLIFVGTVEGVPWSKTGGLGVDVGLGPPALAAARGHVRMTISPRYDQYKDAWDTSVAVEVK 140
QY 61 MG---EKVRYFHSIKKGVHRVWIDHPWFLAKVWGTGSKLYGPRSGADYLDNKKRFALFC 117
DB 141 VGDSTIEVRFHCYKRGVDRVDFVDPHMFLEKVGWGTGSKLYGPKAGLDYLDNLRFSLLC 200
QY 118 KAAEAARVLPF-----GP-GEPCVFVANDHWSALVPVLLKDEYQPKGQFTKAKSVIA 169
DB 201 QAALEAPKVLNLSNYSYSGPVEDVLFANDWHHTALIPCYLKSMSYQSGIYLNKAVFC 260
QY 170 IHNIAFGQRMDEAPFKTKLPQAAFDKLAFSQYAKVYTEATPMEDEKPPLTGTYKKI 229
DB 261 IHNIAFGQRFSDPFLNLDPEFRGSFDFIDGYE-----PVKG---RKI 303
QY 230 NNLKGSIIAADKLVTVSPNYATEINADAAGGVGLDVTIIRAKGIESIVNGMDIEENPKTD 289
DB 304 NNMKAGILSHRVTVSPNYAQELVSAYDKGVGLDSVLRKTCITGIVNGMDTQEWNPATD 363
QY 290 KFLSAPYDQNSYAGKAAKALQALGLPVDPTAPLFAFTGRLEEQGVLDIILALPKI 349
DB 364 KYTDVKYDITTVMDAKPLKALQANGLPVDKTKIPLIGFGRLEEQGSDILVAIIHKF 423
QY 350 LATPKVQIATLGTGKAAVEKLVLNALTGTYKGRKGVKFSAPLAHMLTAGADFMVPSRF 409
DB 424 IGL-DVQIVLVLTGKKEFEQLEQLEVLVLPNKAKGVAFNVLAHMTAGADFMVPSRF 482

QY 410 EPGCLQLHAMHYGTVPVWASTGGLVDTV 438
DB 483 EPGCLQLHAMRYGTVPICASTGGLVDTV 511

RESULT 4

ID UGST_PEA STANDARD; PRT; 603 AA.
AC 043092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11) (GBSSI).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OC NCBI_TaxID=3886;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 76-88.
RC STRAIN=cv. BC1/RR; TISSUE=Embryo;
RX MEDLINE=93251108; PubMed=1302049;
RA Dry I., Smith A., Edwards A., Bhattacharyya B., Dunn P., Martin C.;
RT "Characterization of cDNAs encoding two isoforms of granule-bound
RT starch synthase which show differential expression in developing
RT storage organs of pea and potato.";
RL Plant J. 2:193-202(1992).
CC -!- FUNCTION: MAY BE RESPONSIBLE FOR THE SYNTHESIS OF AMYLOSE.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN PODS AND LEAVES. NO EXPRESSION
CC IN FLOWERS OR STIPULES.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES OF EMBRYONIC
CC DEVELOPMENT WITH HIGHEST LEVELS IN LATER DEVELOPMENTAL STAGES.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; X88789; CAA61268.1; -;
DR InterPro; IPR001296; Glycos.transf.1.
DR Pfam; PF00534; Glycos.transf.1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Starch biosynthesis.
FT TRANSIT 1 75 CHLOROPLAST.
FT CHAIN 76 603 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 91 91 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 603 AA; 66362 MW; 817252FDD12CCAA0 CRC64;
Query Match 55.0%; Score 1258; DB 1; Length 603;
Best Local Similarity 54.9%; Pred. No. 1.6e-82;
Matches 248; Conservative 63; Mismatches 105; Indels 36; Gaps 9;
QY 2 LDIVVAAEVPWSKTGGLGVDVTGGPLTELKVRHVRMTIAPRYDQYADAWDTSVVVDI- 60
DB 77 MSLVFGVEGVPWSKTGGLGVDVGLGPPVLAAGHVRMTVSPRYDQYKDAWDTNVLVEVK 136
QY 61 MGEK---VRYFHSIKKGVHRVWIDHPWFLAKVWGTGSKLYGPRSGADYLDNKKRFALFC 117
DB 137 VGDKLTETVRFHCYKRGVDRVDFVDPHMFLEKVGWGTGSKLYGPKGIDYRDLRFSLLC 196
QY 118 KAAEAARVLPF-----GP-GEPCVFVANDHWSALVPVLLKDEYQPKGQFTKAKSVIA 169
DB 118 KAAEAARVLPF-----GP-GEPCVFVANDHWSALVPVLLKDEYQPKGQFTKAKSVIA 169

```

Db 197 QAALEAPRVNLNSSKYSFGPYGDEVLVAVANDHSAIPVLYKSMYKSRGLYKNAKVAFC 256
QY 170 IHNTAFQGRWEEAFK--TKLPQAFAFKLAFSDGAKYVTEATPMEDEKPLTGTXY 226
Db 257 IHNTAYOGR--NAFSDPSLNLUPDEPRSSDFIDGYNK-----PCEG--- 296
QY 227 KKNLWKGIIAADKLVTVSPNATEIAADAAGVELDTVIRAKGIEGIVNGMDIEEWN 286
Db 297 KKNWMAKAGILESDQVETVSPHYAKELISGEDRGVLDNIIRSGIIVNGMDREWS 356
QY 287 KTKFELAPYDQNSVYAGKAAAEALQAEGLPVDPTAPFAFGRLEEQKGVDIILAAL 346
Db 357 QTRDYIDVHNTEITVETAKPLKGLTQAEIGLPPVDSISPLIGFGRLEEQKGSILVEAI 416
QY 347 PKIILATPKVQIATIGTGKAAVEKLVNAIGTKYGRAGVYKFSAPLAHMLFAGADEMLVP 406
Db 417 AK-FADENVQIVLGTGKKTKNEKQIEVEKYPGKAIGTKFNSPLAKHIIAGADFVIP 475
QY 407 SRPEFCGLIOLHAMHYGTVPVAVSTGGGLVDIV 438
Db 476 SRPEFCGLVOLHAMPYGTVPVLSVSTGGGLVDIV 507

RESULT 5
UGST_IPOBA STANDARD; PRT; 608 AA.
AC Q42857;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11).
GN WAXY OR SS67.
OS Ipomoea batatas (Sweet potato) (Batale).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
OX NCBI_TaxID=4120;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Tainong 57; TISSUE=Tuberous root;
RA Wang S.J., Yeh K.W., Tsai C.Y.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOSYNTHASE
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U4126; AAA86423.1; -.
CC InterPro: IPR001296; Glycos_transf_1.
CC Pfam: PF00534; Glycos_transf_1.
CC KW Glycogen biosynthesis; Transfrase; Glycosyltransferase;
CC KW Transit peptide; Chloroplast; Starch biosynthesis.
CC TRANSIT 1 76 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 77 608 GRANULE-BOUND GLYCOSYNTHASE.
CC FT BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).
CC SEQUENCE 608 AA; 67000 MW; CCA8FA50A2F69CB0 CRC64;

```

Query Match 54.5%; Score 1246; DB 1; Length 608;
 Best Local Similarity 56.3%; Pred. No. 1.1e-81;
 Matches 253; Conservative 48; Mismatches 118; Indels 30; Gaps 7;

```

QY 2 IDIVMAAEVAPWSKTGGGLGVDTGGLPIELVKRGRHVRMTIAPRYDQYADAMDTSVVVD-I 60
Db 82 MNLVFGCEEGPWCKTGGGLGVDTGGLPPALAAARGHRVMTVCPRYDQYKADNETCVVVEPQ 141
QY 61 MG---EKVRYFHSIKKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHKRFALFC 117
Db 142 VGDRIEPPYRFHSYKRGVDRVFDHPMELEKVMGKTSMLYGPAGKDYKONQLRFSLLC 201
QY 118 KAAEAAARVLPF-----GP-GEPCVFVANDHSAIPVLLKDEYQPKGQFTAKSVLA 169
Db 202 QAALEAPRVNLNSSKYSFGPYGDEVLVAVANDHSAIPVLYKSMYKSRGLYKNAKVAFC 261
QY 170 IHNTAFQGRWEEAFKTKLPQAFAFKLAFSDGAKYVTEATPMEDEKPLTGTGTYYKI 229
Db 262 IHNTAYOGRFAFSDFSLLNLPDEYKGSDFIDGYNK-----PVKG---RKI 304
QY 230 NWLKGGIIAADKLVTVSPNATEIAADAAGVELDTVIRAKGIEGIVNGMDIEEWNPKTD 289
Db 305 NWMKAGITREARVFTVSPNAYAKELVSCVSKGVDELNDHDCGICITGCMGDTQENWPAID 364
QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPFAFGRLEEQKGVDIILAALPKI 349
Db 365 KYLAVKYDITVVMQAKPLKALQAAVGLPVDNRNIPLIIGFGRLEEQKGSILYAAISKF 424
QY 350 LATPKVQIATIGTGKAAVEKLVNAIGTKYGRAGVYKFSAPLAHMLFAGADEMLVPSRF 409
Db 425 ISM-DVQITLILGTGKKFEQQLQEVNMYPKARGVAKENVPLAHMITAGADFMLIPSRF 483
QY 410 EPCGLIOLHAMHYGTVPVAVSTGGGLVDIV 438
Db 484 EPCGLIOLHAMRYGIPCAISGGLVDIV 512

RESULT 6
UGST_HORVU STANDARD; PRT; 603 AA.
AC P09842;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11).
GN WAXY.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Vogelsanger Gold; TISSUE=Leaf;
RA MEDLINE=88303345; PubMed=2970062;
RX Rhode W., Becker D., Salamini F.;
RT "Structural analysis of the waxy locus from Hordeum vulgare.";
RL Nucleic Acids Res. 16:7185-7186(1988).
RN [2]
RP SEQUENCE OF 76-89.
RC STRAIN=cv. H354-295-2-5; TISSUE=Starchy endosperm;
RX MEDLINE=94170739; PubMed=8125056;
RA Flengsrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional
RT electrophoresis.";
RL Electrophoresis 14:1060-1066(1993).
CC -!- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOSYNTHASE
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U4126; AAA86423.1; -.
CC InterPro: IPR001296; Glycos_transf_1.
CC Pfam: PF00534; Glycos_transf_1.
CC KW Glycogen biosynthesis; Transfrase; Glycosyltransferase;
CC KW Transit peptide; Chloroplast; Starch biosynthesis.
CC TRANSIT 1 76 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 77 608 GRANULE-BOUND GLYCOSYNTHASE.
CC FT BINDING 96 96 UDP-GLUCOSE (BY SIMILARITY).
CC SEQUENCE 608 AA; 67000 MW; CCA8FA50A2F69CB0 CRC64;

```



```

Db 484 EPCGLIQGMRYTGPCACASTGGLVDTI 512

RESULT 11
UGST_MAIZE STANDARD; PRT; 605 AA.
AC P04713;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granule-bound glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11).
GN WAXY.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Kioesgen R.B., Gierl A., Schwarz-Sommer Z., Saedler H.;
RT "Molecular analysis of the waxy locus of Zea mays.";
RL Mol. Gen. Genet. 203:237-244(1986).
CC -!- FUNCTION: REQUIRED FOR THE SYNTHESIS OF AMYLOSE IN ENDOSPERM.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST, GRANULE-BOUND.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X03935; CAA27574.1; -
DR EMBL; M24258; AAA33520.1; -
DR PIR; S07314; S07314.
DR MaizeDB; 15806; -
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Starch biosynthesis.
FT TRANSIT 1 72 CHLOROPLAST.
FT CHAIN 73 605 GRANULE-BOUND GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 91 91 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 605 AA; 65966 MW; 137F15207DBFC189 CRC64;

Query Match 51.8%; Score 1185; DB 1; Length 605;
Best Local Similarity 52.0%; Pred. No. 2.6e-77;
Matches 234; Conservative 67; Mismatches 119; Indels 30; Gaps 8;

QY 2 LDIWVAEAVPWSKTGGLGVDTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVYVDI- 60
Db 77 MNVVFVGAEMAPWSKTGGLGVDTGGLPLPMAANGHRVMVSPRYDQYKDAWDTSVVSEIK 136
QY 61 MG---EKVRYPHSKKGVRHVRWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHKFAFLFC 117
Db 137 MGDYEIVRFPHCYKRGVDRVFDVDPFLFLEKRVGKTEKIKYGPVAGTDYRDNQRLFSLLC 196
QY 118 KAAIEAARVL-----PF--GPG-EDCVFVANDHSAIPLVLLKDEYQPKGQFTAKSVLA 169
Db 197 QAALAEAPRLSLNNPFSGPGYEDVFEVCNDWHTGPLSCYLKSNYQSHGIYRDAKATFC 256
QY 170 IHNIAFCQRMEEAFKDKLPQAADFCLAFSDGAKVYTEATPMEEDKPLTKYTKKI 229
Db 257 IHNISYQGRFAFSYDPELNLNLPFRPKSSFDIDGYEK-----PVEG---RKI 299
QY 230 NWLKGIIIAADKLVTVSPNYATEIAADAAGGVDELDTVIRAKGIEGIVNGMDEEWNPKTD 289

```

```

Db 300 NNMKAGILEADRVLTSPYYAEELISGARGELDNIMRLTGITVINGMDYSEWDPSRD 359
QY 290 KFLSAPYDONSVYAGKAAKALQAEGLGLPVLPTAPLEAFIGRLERQKGVDIILAALPKI 349
Db 360 KYIAKYDVSTAVEAKALNKEALQAEVGLPVNRNIPLVAFIGRLERQKGPVMAAIIQL 419
QY 350 L-ATPKVQITAILGTGKAAYEKLVNAIGTKYKRAKGVVVKFSAPLAHMLTAGADEMLVPSR 408
Db 420 MEMVEDVQIVLLGTGKKKFERMLMSAEKFPCKVRVAVKFNAAALAHMAGADVLAITSR 479
QY 409 FEPCCGLIQHAMHYGTVPVVASTGGLVDTV 438
Db 480 FEPCCGLIQGMRYTGPCACASTGGLVDTI 509

RESULT 12
UGS2_SOLTU STANDARD; PRT; 641 AA.
AC P93568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Soluble glycogen [starch] synthase, chloroplast precursor
DE (EC 2.4.1.11) (SS I).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-cv. Desiree; TISSUE=Leaf;
RT MEDLINE=97164391; PubMed=9011082;
RA Abel G.J.W., Springer F., Willmitzer L., Kossmann J.;
RT "Cloning and functional analysis of a cDNA encoding a novel 139 kDa
RT starch synthase from potato (Solanum tuberosum L.)";
RL Plant J. 10:981-991(1996).
CC -!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-alpha-D-glucosyl}(N) =
CC UDP + {(1,4)-alpha-D-glucosyl}(N+1).
CC -!- PATHWAY: Starch biosynthesis.
CC -!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y10416; CAA71442.1; -
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase;
KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
FT TRANSIT 1 641 ? CHLOROPLAST (POTENTIAL).
FT CHAIN 145 145 SOLUBLE GLYCOGEN [STARCH] SYNTHASE.
FT BINDING 145 145 UDP-GLUCOSE (BY SIMILARITY).
SQ SEQUENCE 641 AA; 70608 MW; 30FB0546CFB74C CRC64;

Query Match 38.0%; Score 870.5; DB 1; Length 641;
Best Local Similarity 42.9%; Pred. No. 8.2e-55;
Matches 194; Conservative 80; Mismatches 139; Indels 39; Gaps 14;

QY 3 DIVWVAEAVPWSKTGGLGVDTGGLPIELVKRGHRVMTIAPRY-----DOYADAWDT 55
Db 132 NIIFVTAAAPYSKTGGLGVDTGGLPMAALAAFGHRVMVSPRYLNGGSPDEKYANAVDLD 191
QY 56 V--VVDIMG--EKVRYFHSIKKGVRHVRWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHK 111

```

Db 192 VRATVCFGDAEVAFYHEIRAGVDFVDFHSSYC-----RPGTP-YGDIYA-FGDNOF 244
 QY 112 RFALFCKAATRAARVLPPGP---GEDCVFVANDHWSALVPVLLKDEYOPKGOFTKAKSVL 168
 Db 245 RFTLLSHAACEAPLVLPLGGTGYEKCLFLANDHAALVPLLLAAKRYPGYVKDARSIV 304
 QY 169 AHNIAFOGRWEEAFKOTKLPQAAFDKLAFSDGAKVYTEATPMEDEKPLTKTKYK 228
 Db 305 AHNIAHOGVEPAVYNNIGLPPQWYGAV---EWIFPTWARAHALD-----TGET--- 351
 QY 229 INWLKGGIIAADKLVTSPNATETAADAAGVDELDTVI--RAKIGIEIVNGMDIEENP 286
 Db 352 VNLKGAITAVADRILTVSQYSWEITP-PEGYGLHELLSSQSVLNGITNGIDVNDWP 410
 QY 287 KTDKELSPYQNSVYAGKAAKAEALQAEGLPVDPTAPLFAFICRLEEQKGVDIILAA 346
 Db 411 STDEHIAHSYINDL-SGVQCKTDLQKELGLPIRDCPLIGFICRGLDYQKGVDIILSAI 469
 QY 347 PKILATPKVQIAILGTGKAAEKLVAIGTKYGRKGVKFSAPLAHMLTAGADFMVLP 406
 Db 470 PELMQN-DVQVVLGSGEKQEDWMHTENLFDKFRWVGFPVSHRITAGCDLILMP 528
 QY 407 SRFEPCGLIQLHAMHYGTVPVASTGGLVDIV 438
 Db 529 SRFEPCGLNQLYAMRYGIPVHSVGGGLVDIV 560

RESULT 13
 UGS2_ORYZA
 ID UGS2_ORYZA STANDARD; PRT; 626 AA.
 AC Q40739;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Soluble glycogen [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11) (SSS)
 OS Oryza sativa (Rice)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 114-131.
 RC STRAIN=cv. Japonica; TISSUE=Seed;
 EX MEDLINE=94302151; PubMed=7518089;
 RA Baba T., Nishihara M., Mizuno K., Kawasaki T., Shimada H.,
 RA Kobayashi E., Onishi S., Tanaka K.-I., Arai Y.;
 RT "Identification, cDNA cloning, and gene expression of soluble starch
 RT synthase in rice (Oryza sativa L.) immature seeds.";
 RL Plant Physiol. 103:565-573(1993).
 CC -!- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
 CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
 CC -!- PATHWAY: starch biosynthesis.
 CC -!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE.
 CC -!- TISSUE SPECIFICITY: LEAVES AND IMMATURE SEEDS.
 CC -!- MISCELLANEOUS: THREE FORMS OF SOLUBLE STARCH SYNTHASE WERE
 CC PURIFIED: RSS1, RSS2 AND RSS3.
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
 CC FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D16202; BAA03739.1; -
 CC InterPro; IPR001296; Glycos_transf_1.
 CC Pfam; PF00534; Glycos_transf_1; 1.
 CC Glycogen biosynthesis; Transferase; Glycosyltransferase;
 CC

KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
 FT TRANSIT 1 113 CHLOROPLAST (POTENTIAL).
 FT CHAIN 114 626 SOLUBLE GLYCOGEN [STARCH] SYNTHASE, RSS3.
 FT CHAIN 122 626 SOLUBLE GLYCOGEN [STARCH] SYNTHASE, RSS1.
 FT BINDING 147 147 UDP-GLUCOSE (BY SIMILARITY).
 SQ SEQUENCE 626 AA; 68451 MW; 03E4182507D26658 CRC64;
 Query Match 38.0%; Score 870; DB 1; Length 626;
 Best Local Similarity 42.7%; Pred. No. 8.6e-55;
 Matches 192; Conservative 74; Mismatches 146; Indels 38; Gaps 12;
 QY 4 IYVVAEAVAPSKTGGGLDVTGGLPTELKVRHVMTIAPRY-----DOYADANDTSV 57
 Db 135 VYVFTGEASPYAKSGGLGDCVCSLPALALGRHVMVMPRYMNGALNKNFANAFYTERH 194
 QY 58 VDIM---GE-KYRIFHSIKKGVHRYWIDHPWELAKVWGKTSGLYGPSCADYLDNHKRF 113
 Db 195 IKIPCFGSEHEVTFEYKDSVDWVVDHPSTY-----HRPNLYGDNFGA-FGDNQF 247
 QY 114 ALFCKAAATEAARVLPPGP---GEDCVFVANDHWSALVPVLLKDEYOPKGOFTKAKSVLAI 170
 Db 248 TLLCYAACEAPLILELGGVYIGKCMFVVDHWSALVPVLLAAKRYPGYVYRDSRVLI 307
 QY 171 HNIATQGRWEEAFKDTKLPQAAFDKLAFSDGAKVYTEATPMEDEKPLTKTKYKKN 230
 Db 308 HNLHOGVEPASTYDPLGLPPEWYGALEW-----VFPEWARRHALDKG-----EAVN 354
 QY 231 WLKGGIIAADKLVTSPNATETAADAAGVDELDTVI--RAKIGIEIVNGMDIEENPDKT 288
 Db 355 FLKGAVTVADRILTVSQYSWEITP-PEGYGLHELLSSQSVLNGITNGIDVNDWPST 413
 QY 289 DKFLSAPYQNSVYAGKAAKAEALQAEGLPVDPTAPLFAFICRLEEQKGVDIILAAALPK 348
 Db 414 DKFLPYHYSVDL-SGAKCAELQKELGLPIRDPVPLIGFICRGLDYQKGVDIILKLAIPD 472
 QY 349 ILATPKVQIAILGTGKAAEKLVAIGTKYGRKGVKFSAPLAHMLTAGADFMVPSR 408
 Db 473 LM-RDNIQFVLMGSDGDFEGMWRSTESGDKFRGVGFSVPVSHRITAGCDLILMPSR 531
 QY 409 FEPCLQLQLHAMHYGTVPVASTGGLVDIV 438
 Db 532 FEPCLNQLYAMRYGIPVHSVGGGLVDIV 561

RESULT 14
 UGS2_WHEAT
 ID UGS2_WHEAT STANDARD; PRT; 610 AA.
 AC Q43654;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Soluble glycogen [starch] synthase, chloroplast precursor
 DE (EC 2.4.1.11) (Fragment).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. T.A. Florida; TISSUE=Endosperm;
 RA Block M., Loez H., Luetticke S.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
 CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
 CC -!- PATHWAY: starch biosynthesis.
 CC -!- SUBCELLULAR LOCATION: AMYLOPLAST OR CHLOROPLAST, SOLUBLE (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
 CC FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: U48227; AAB02197.1; -.
 DR InterPro: IPR001296; Glycos_transf_1.
 DR Pfam: PF00534; Glycos_transf_1.
 KW Glycogen biosynthesis; Transferease; Glycosyltransferase;
 KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
 FT NON_TER 1
 FT TRANSIT 1
 FT CHAIN 1
 FT BLINDING 7
 FT SEQUENCE 610 AA; 67143 MW; 46080A3B7F87193 CRC64;

Query Match 37.2%; Score 850; DB 1; Length 610;
 Best Local Similarity 43.0%; Pred. No. 2.2e-53;
 Matches 191; Conservative 71; Mismatches 144; Indels 38; Gaps 12;

QY 10 EVAPWSKTGGLGVDVTGGLPIELVKRGHVRMTIAPRY-----DOYADAWDTSVVVDIM-- 61
 DB 1 EAAPYAKSGGLGVDVCGSLPATAARGHVRVMPVPRYLNGSSDKNYAKALYAKHIKIPCF 60
 QY 62 --GEKRYPHSIRKGVHVRWIDPFLAKVWGKTGSKLYGPRSGADYLDNHRKFALECKA 119
 DB 61 GGSHEVTFEYRDNVDWVFDHP-----SYHRPGS-LYGDNFGA-FGDNQFRYLLCYA 113
 QY 120 AIEARVLPFGP---GEDCVFVANDHSAIVPVLKDEYOPKGOFTKAKSVLAHNAFQ 176
 DB 114 ACEAPLILELGGYTYGNCMFVNDHSAIVPVLKDEYOPKGOFTKAKSVLAHNAFQ 173
 QY 177 GRMWEAFKTKLPQAAFDKLAISDGYAKVYVTEATPMEDEKPLTKTKYKINWLKGI 236
 DB 174 GVEPASTYDGLPPEWYGALEW-----VFPWARHRLDKG-----EAVNFKGAV 220
 QY 237 IAAKLVTVSPNYATEIAADAAGGVLDTVI--RAKGIEGIVNGMDIEENPKTKPLISA 294
 DB 221 VTADRIVTVSGQSWYETI--AEGSQGLNELLSSRKSVLNGVINGIDINDWNTPTDKCLPH 279
 QY 295 PYDONSIVYAGAAKAEALQELGLPVDPTAPLFAFGRLEQKGVLDIILALPKILATPK 354
 DB 280 HYSVDDI--SGKAKC-KAELOKELGLPVREDVPLIGFGLKDYOKGIDILKMAIPELM-RED 337
 QY 355 VQIATLGTGAAYEKLVNAIGTKYKRAKGVKVFSAFLAHMLTAGADFMVPSRFEPCGL 414
 DB 338 VQFVNLGSGDPFEGWRSSTESSYKDKFERGWGVSFVPSHRIITAGCDILLMPSRFEPCGL 397
 QY 415 IQLHAMHYGTVPVVGSTGLVDIV 438
 DB 398 NQLYAMQYGTVPVVGSTGLVDIV 421

RESULT 15
 UGS3_PEA
 ID UGS3_PEA
 AC Q43093; STANDARD; PRT; 752 AA.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Glycogen [starch] synthase, chloroplast precursor (EC 2.4.1.11)
 DE (GBSSI) (granule-bound starch synthase II).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsid I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 58-73.
 RC STRAIN=cv. BCL/RR; TISSUE=Embryo;
 RX MEDLINE=93251108; PubMed=1302049;
 RA Dry I., Smith A., Edwards A., Bhattacharyya B., Dunn P., Martin C.;

RT "Characterization of cDNAs encoding two isoforms of granule-bound
 RT starch synthase which show differential expression in developing
 RT storage organs of pea and potato.";
 RL Plant J. 2:193-202(1992).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + ((1,4)-alpha-D-glucosyl)(N) =
 CC UDP + ((1,4)-alpha-D-glucosyl)(N+1).
 CC -1- PATHWAY: Starch biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST/AMYLOPLAST, SOLUBLE AND GRANULE-
 CC BOUND.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- DEVELOPMENTAL STAGE: MOST HIGHLY EXPRESSED IN EARLY EMBRYOS.
 CC LEVELS DECLINE IN LATER STAGES OF DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
 CC FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: X89790; CAA61269.1; -.
 DR InterPro: IPR001296; Glycos_transf_1.
 DR Pfam: PF00534; Glycos_transf_1.
 KW Glycogen biosynthesis; Transferease; Glycosyltransferase;
 KW Transit peptide; Chloroplast; Amyloplast; Starch biosynthesis.
 FT TRANSIT 1
 FT CHAIN 58
 FT BLINDING 275
 FT SEQUENCE 752 AA; 83617 MW; E0496420CD359395 CRC64;

Query Match 36.4%; Score 833; DB 1; Length 752;
 Best Local Similarity 41.8%; Pred. No. 4.8e-52;
 Matches 189; Conservative 73; Mismatches 142; Indels 48; Gaps 12;
 QY 2 LDIWVAEAVAPWSKTGGLGVDVTGGLPIELVKRGHVRMTIAPRYDOYADAWDTSV--VVD 59
 DB 261 MNILVSAECAPWSKTGGLGVDVAGSLPKALARRGHVRVMPVPRYLNGSSDKNYAKALYAKHIKIPCF 320
 QY 60 IMGE--KVRYPHSIRKGVHVRWIDPFLAKVWGKTGSKLYGPRSGADYLDNHRKFALECKA 117
 DB 321 VAGDMEVTFEYRDNVDWVFDHP-----IFRMESNYI-----GGNELDLIRMWLFC 371
 QY 118 KAAIEAARVLP-----FGGEDCVFVANDHSAIVPVLKDEYOPKGOFTKAKSVLAHNA 172
 DB 372 KAAVEVPHVPCGGICYGDG-NLVPFIANDWHTALLPVYLKAYVDRHGLMNTVRSVLVHNA 430
 QY 173 IAFQGRWEEAFKTKLPQAAFDKLAISDGYAKVYVTEATPMEDEKPLTKTKYKINWL 232
 DB 431 IAHQGRG-----EVEDFTVLDLGNLDFKMYDPVGGH-----FNIF 469
 QY 233 KGGIATAADKLVTVSPNYATEIAADAAGGVLDTVIRAKG--IEGIVNGMDIEENPKTKD 290
 DB 470 AAGLKATADRIVTVSHGYAWELKT-SEGWGLNLIINESDKWFRGIVNGVDIKWNPQFDA 528
 QY 291 FLSAP-----YDONSIVYAGAAKAEALQELGLPVDPTAPLFAFGRLEQKGVLDIILAL 346
 DB 529 YLTSFGYTNLTKLTQTKRQCKAALQRELGLPVREDVPLIISFIRGLDHQKGVLDIAEAI 588
 QY 347 PKILATPKVQIATLGTGAAYEKLVNAIGTKYKRAKGVKVFSAFLAHMLTAGADFMVLP 406
 DB 589 PWM--SHDVLQVLMUGTGRADLEQMLKEFEAQHCDKIRSWGVSFVMAHRIITAGSDILLMP 647
 QY 407 SRFEPCGLIQLHAMHYGTVPVVGSTGLVDIV 438
 DB 648 SRFEPCGLNQLYAMSYGIVPVVHGVGGLRDTV 679

Search completed: June 4, 2003, 14:53:22
 Job time : 10.8812 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:35:26 ; Search time 21.7603 Seconds
(without alignments)
4147.394 Million cell updates/sec

Title: US-09-980-771A-7
Perfect score: 2288
Sequence: 1 ALDIVMAEVAEPAWSKTGGL.....AMHYGTVFVASTGGLVDTV 438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2284	99.8	708	10	064925
2	1282	56.0	613	10	093YB1
3	1275	55.7	604	10	09FR03
4	1261	55.1	608	10	093VD9
5	1254	54.8	607	10	092S05
6	1250	54.6	606	10	09XIS6
7	1242	54.3	610	10	09MAQ0
8	1232.5	53.9	603	10	08SA49
9	1229	53.7	609	10	094LY7
10	1221.5	53.4	605	10	09SXX3
11	1221.5	53.4	605	10	09FUU6
12	1221	53.4	609	10	08S9C4
13	1217.5	53.2	604	10	09SL56
14	1216.5	53.2	574	10	09SYU0
15	1216.5	53.2	604	10	09S7N5
16	1214.5	53.1	608	10	08YU1

17	1212.5	53.0	534	10	08W2G8
18	1211.5	53.0	599	10	09SQ58
19	1210.5	52.9	606	10	043012
20	1209.5	52.9	604	10	09SL57
21	1208.5	52.8	605	10	09SQ51
22	1207.5	52.8	605	10	09SL58
23	1204.5	52.6	604	10	09SXX4
24	1202.5	52.6	604	10	09SL59
25	1197.5	52.3	605	10	09SQ52
26	1105.5	48.3	565	10	09XEN9
27	895.5	39.1	313	10	09LKD3
28	893.5	39.1	313	10	09LKE0
29	893.5	39.1	313	10	09FYU8
30	886.5	38.7	313	10	09LKE8
31	885.5	38.7	313	10	09LKD1
32	879.5	38.4	313	10	09LKE5
33	879.5	38.4	313	10	09LKD6
34	878.5	38.4	313	10	09LKE7
35	878.5	38.4	313	10	09LKE1
36	877.5	38.4	313	10	09LKD8
37	877.5	38.4	313	10	09LKE5
38	876.5	38.3	313	10	09LKE5
39	876.5	38.3	313	10	09LKE4
40	875.5	38.3	313	10	09LKE2
41	874.5	38.2	313	10	09LKE3
42	874.5	38.2	313	10	09LKE2
43	873.5	38.2	313	10	09LKE6
44	870.5	38.0	313	10	09LKD4
45	870	38.0	623	10	09SSY9

ALIGNMENTS

RESULT 1

064925
ID 064925 PRELIMINARY: PRT; 708 AA.
AC 064925

DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Granule-bound starch synthase I precursor (EC 2.4.1.21).
GN StA2.

OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
CX NCBI_taxID=3055;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=137C;
RA D'Hulst C., Watebled F., Ral J.-P., Abel G.J., Kossmann J.,
RA Ball S.G.;
RT "Cloning of a cDNA encoding for the GBSI in the green alga
Chlamydomonas reinhardtii.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RA Watebled F., Ball S.G., D'Hulst C.;
RT "Granule-bound starch synthase I: A major enzyme involved in the
biogenesis of B-crystallites in starch granules.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF026420; AAC17969.3; -
DR EMBL: AF433156; AAL28128.1; -
DR InterPro: IPR001296; Glycosyltransf_1.
DR InterPro: IPR002114; HPR_SerP_site.
DR Pfam: PF00534; Glycosyltransf_1; 1.
DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
DR Glycosyltransferase; Transferase; Transit peptide.
FT TRANSIT 1 57 POTENTIAL.
FT CHAIN 58 708 GRANULE-BOUND STARCH SYNTHASE I.
SQ SEQUENCE 708 AA; 74623 MW; 7D2A5A07D8606469 CRC64;

Query Match

99.8%; Score 2284; DB 10; Length 708;

```

Best local similarity 99.8%; Pred. No. 3.4e-166;
Matches 437; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALDIVVAEVAAPWSKTTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI 60
Db 58 ALDIVVAEVAAPWSKTTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI 117
QY 61 MGEKRVYFHSIKKGVRHWIDHPWFLAKVWKGTSKLYGPRSGADYLDNHRKRALFC 120
Db 118 MGEKRVYFHSIKKGVRHWIDHPWFLAKVWKGTSKLYGPRSGADYLDNHRKRALFC 177
QY 121 IEAARVLPFGPGEDCVFVANDHWSALVPVLLKDEYQPKGQFTAKSVLAIHNTAFQGRMW 180
Db 178 IEAARVLPFGPGEDCVFVANDHWSALVPVLLKDEYQPKGQFTAKSVLAIHNTAFQGRMW 237
QY 181 EAFKDTKLPQAAFDKLPASDGYAKVYVTEATPMEDEKPLTGKTKYKINWLGKGIITAD 240
Db 238 EAFKDTKLPQAAFDKLPASDGYAKVYVTEATPMEDEKPLTGKTKYKINWLGKGIITAD 297
QY 241 KLTVSPNYATEIAADAAGVELDTVIRAKGIEGIVNGMDIEENPKTDKFLSAPYDQNS 300
Db 298 KLTVSPNYATEIAADAAGVELDTVIRAKGIEGIVNGMDIEENPKTDKFLSAPYDQNS 357
QY 301 VYAGKAAKALQAEGLPVDPTAPLPAFTGRLEEQKGVDDIILAAALPKILATPKVQITAIL 360
Db 358 VYAGKAAKALQAEGLPVDPTAPLPAFTGRLEEQKGVDDIILAAALPKILATPKVQITAIL 417
QY 361 GTGKAAVEKLVNAIGTKYGRAGVWKFSAPLAHLTAGADEMLVPSRFEPCGLIQLHAM 420
Db 418 GTGKAAVEKLVNAIGTKYGRAGVWKFSAPLAHLTAGADEMLVPSRFEPCGLIQLHAM 477
QY 421 HYGTVPVVASTGGGLDVT 438
Db 478 HYGTVPVVASTGGGLDVT 495

RESULT 2
Q93YB1 ID Q93YB1 PRELIMINARY; PRT; 613 AA.
AC Q93YB1:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE Granule-bound starch synthase (EC 2.4.1.11).
GN GBSSI.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Edwards A., Vincken J.P., Visser R., Zeeman S., Smith A.M., Martin C.;
RT "Discrete forms of amylose are synthesised by isoforms of GBSSI in pea.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ345045; CAC69955.1; -.
DR InterPro; IPR001296; Glycos.transf.1.
DR InterPro; IPR001917; Ntrtransf.2.1.
DR Pfam; PF00534; Glycos.transf.1.
DR PROSITE; PS00599; AA_TRANSF_CLASS_2; UNKNOWN.1.
KW Glycosyltransferase; Transferase; Transit peptide.
FT TRANSIT 1 85
FT CHAIN 86 613 GRANULE BOUND STARCH SYNTHASE.
SQ SEQUENCE 613 AA; 67626 MW; 5A653461128F97EB CRC64;

Query Match 56.0%; Score 1282; DB 10; Length 613;
Best Local Similarity 55.8%; Pred. No. 1.4e-89;
Matches 252; Conservative 58; Mismatches 106; Indels 36; Gaps 8;

QY 2 LDIVMVAEVAAPWSKTTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI- 60
Db 78 MTLIFVSAECGPGWSKTTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI- 137
QY 61 MGEKVR---YFHSIKKGVRHWIDHPWFLAKVWKGTSKLYGPRSGADYLDNHRKRALFC 117
Db 138 VGDKVETVGFPCYKRGVDRVDFHPLFLEKYGWTKSKVYGPSAGVDYEDNQLRFLS 197
QY 118 KAAIEAARVLPF-----GP-GEDCVFVANDHWSALVPVLLKDEYQPKGQFTAKSVLA 169
Db 198 LAALEAPRVNLNTSNKYFSGPYCEDVVFVANDHWTAVLPCYKTIYQPKGIYTNKAVLIC 257

Best local similarity 99.8%; Pred. No. 4.6e-89;
Matches 256; Conservative 51; Mismatches 112; Indels 30; Gaps 7;

QY 2 LDIVMVAEVAAPWSKTTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI- 60
Db 78 MTLIFVSAECGPGWSKTTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI- 137
QY 61 MGEKVR---YFHSIKKGVRHWIDHPWFLAKVWKGTSKLYGPRSGADYLDNHRKRALFC 117
Db 138 VGDKVETVGFPCYKRGVDRVDFHPLFLEKYGWTKSKVYGPSAGVDYEDNQLRFLS 197
QY 118 KAAIEAARVLPF-----GP-GEDCVFVANDHWSALVPVLLKDEYQPKGQFTAKSVLA 169
Db 198 LAALEAPRVNLNTSNKYFSGPYCEDVVFVANDHWTAVLPCYKTIYQPKGIYTNKAVLIC 257

Db 87 MNLIFVTEVAPWSKTTGGGLDVTGGLPALASGHRVMTVTPRDQYKDAWDTNVTIEVK 146
QY 61 ---MGEKRVYFHSIKKGVRHWIDHPWFLAKVWKGTSKLYGPRSGADYLDNHRKRALFC 117
Db 147 VGDTEKVRFEHCFKRGVDRVDFHPLFLEKYGWTKGKLYGPAAGDDYQDNQLRFSIFC 206
QY 118 KAAIEAARVLPF-----GP-GEDCVFVANDHWSALVPVLLKDEYQPKGQFTAKSVLA 169
Db 207 QAALEAARVNLNLSKNSYFSGPYGEDVIFVANDHWTALISCYMKSMYQSIGIFRKAUVFC 266
QY 170 IHNITAFQGRWEEAFKID---TKLPQAAFDKLPASDGYAKVYVTEATPMEDEKPLTGKTY 226
Db 267 IHNITAFQGRWEEAFKID---TKLPQAAFDKLPASDGYAKVYVTEATPMEDEKPLTGKTY 306
QY 227 KKNLWLGKGIITADKLTVSPNYATEIAADAAGVELDTVIRAKGIEGIVNGMDIEENPK 286
Db 307 RKINMKAGIIESHRLVTSVYQAELVSGDPKVELDNLNLRVGVTVGIVNGMDVQEWNP 366
QY 287 KTDKFLSAPYDQNSVYAGKAAKALQAEGLPVDPTAPLPAFTGRLEEQKGVDDIILAAAL 346
Db 367 STDKYISIKYDASTVLESGKALLKELOAEVGLPVDKKNVPLLAFTGRLEEQKGSOLLVEAI 426
QY 347 PKILATPKVQITAILGTGKAAVEKLVNAIGTKYGRAGVWKFSAPLAHLTAGADEMLVP 406
Db 427 PQFT-KENVQIVALTGCKENKQLQLEISYDPKARGVAKENYFLAHLTAGADFILIP 485
QY 407 SRFEPCGLIQLHAMHYGTVPVVASTGGGLDVT 438
Db 486 SRFEPCGLIQLQAMRYGTVPIVASTGGGLDVT 517

RESULT 3
Q9FR03 ID Q9FR03 PRELIMINARY; PRT; 604 AA.
AC Q9FR03:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE Granule-bound starch synthase.
GN GBSSI.
OS Perilla frutescens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteridaceae; euasterids I; Lamiales; Lamiaceae; Perilla.
OX NCBI_TaxID=48386;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. OKDONG; TISSUE=DEVELOPING SEEDS;
RA Hwang S.-K., Hwang Y.-S.;
RT "Isolation and characterization of a cDNA encoding granule-bound starch synthase from Perilla frutescens.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210699; AAG43519.1; -.
DR InterPro; IPR001296; Glycos.transf.1.
DR Pfam; PF00534; Glycos.transf.1.
SQ SEQUENCE 604 AA; 66214 MW; 435CE9601C85A5EF CRC64;

Query Match 55.7%; Score 1275; DB 10; Length 604;
Best Local Similarity 57.0%; Pred. No. 4.6e-89;
Matches 256; Conservative 51; Mismatches 112; Indels 30; Gaps 7;

QY 2 LDIVMVAEVAAPWSKTTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI- 60
Db 78 MTLIFVSAECGPGWSKTTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVVDI- 137
QY 61 MGEKVR---YFHSIKKGVRHWIDHPWFLAKVWKGTSKLYGPRSGADYLDNHRKRALFC 117
Db 138 VGDKVETVGFPCYKRGVDRVDFHPLFLEKYGWTKSKVYGPSAGVDYEDNQLRFLS 197
QY 118 KAAIEAARVLPF-----GP-GEDCVFVANDHWSALVPVLLKDEYQPKGQFTAKSVLA 169
Db 198 LAALEAPRVNLNTSNKYFSGPYCEDVVFVANDHWTAVLPCYKTIYQPKGIYTNKAVLIC 257

```


QY 170 IHNIAQGRWMEAFKDKLPQAADFCLAFSDGAKVYTEATPMEDEKPLTKGTYKKI 229
 Db 258 IHNIAQGRWMEAFKDKLPQAADFCLAFSDGAKVYTEATPMEDEKPLTKGTYKKI 300
 QY 230 NWLKGIIAADKLVTSPNYATEIAADAAGGVVELDTVIRAKGIEGIVNGMDIEENPKTD 289
 Db 301 NNMKAGIESDRVTVSPYANELVSGPDGVVELDNILRKCVITGVNGMDTQEWNPAD 360
 QY 290 KFLSAPYDONSYYAGKAAKEALQAEGLGVPDPTAPLFAFAGRLERQKGVDIILALPKI 349
 Db 361 KYIDNHVITDITVMQAKPLKKEALQAEGLGVPDPTAPLFAFAGRLERQKGVDIILALPKI 420
 QY 350 LATPKVQIAILGTGKAAVEKLVNAIGTKYKGRAGVVKFSAPLAHLMTAGADFMVPSRF 409
 Db 421 IEM-DVQVILGTGKKEFEQTEQLEELYPKAVGVAKFNPVLAHMTAGADFMVPSRF 479
 QY 410 EPCGLIQLHAMHYGTVPVASTGGLVDTV 438
 Db 480 EPCGLIQLHAMRYGTIPICASTGGLVDTV 508

RESULT 4

Q93VD9 PRELIMINARY; PRT; 608 AA.
 AC Q93VD9;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Granule-bound starch synthase I (EC 2.4.1.21).
 GN GBSSI.
 OS Ipomoea batatas (Sweet potato) (Batate).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
 OX NCBI_TaxID=4120;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. KOKEI 14;
 RA Kimura T., Ideta O., Saito A.;
 RT "Identification of the gene encoding granule-bound starch synthase I
 in sweet potato (Ipomoea batatas (L.) Lam.).";
 RL Plant Biotechnol. 17:247-252(2000).
 DR EMBL; AB071976; BAB68525.1; -.
 DR EMBL; AB071604; BAB68126.1; -.
 DR InterPro; IPR001296; Glycosyltransf_1.
 DR Pfam; pf00534; Glycosyltransf_1; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 608 AA; 66689 MW; C93CDA49A1F50C03 CRC64;

Query Match 55.1%; Score 1261; DB 10; Length 608;
 Best Local Similarity 56.8%; Pred. No. 5.4e-88;
 Matches 255; Conservative 48; Mismatches 116; Indels 30; Gaps 7;
 QY 2 LDIYVAAEAVAPWSKTGGLGVDVGTGGLPIELVKRHRVMTIAPRYDOYADAWDTSVVVDI- 60
 Db 82 MNLVFGVGAEGVPSKGTGLGDLVGLGPPALAGNGHRVMTSPRYDQYKDAWDTGVSVEIK 141
 QY 61 MG---EKVRYPHSIKKGVRVWIDHPWFLAKVWGKTKGSKLYGPRSGADYLDNHRKRALFC 117
 Db 142 VGDIEVPFRFHSYKRGVDRVVDHPMFLKRVKWKTKGSKLYGPRSGADYLDNHRKRALFC 201
 QY 118 KAAIEAARVLPF-----GP-GEDCVFVANDHSAHPVLLKDEYQPKGQFTAKSVLA 169
 Db 202 QAALEAPRVNLNNSNYSFSGPYGEDVVFVANDHHTALLPCYLKTMYSRGIYNNKAVFC 261
 QY 170 IHNIAQGRWMEAFKDKLPQAADFCLAFSDGAKVYTEATPMEDEKPLTKGTYKKI 229
 Db 262 IHNIAQGRWMEAFKDKLPQAADFCLAFSDGAKVYTEATPMEDEKPLTKGTYKKI 304

QY 230 NWLKGIIAADKLVTSPNYATEIAADAAGGVVELDTVIRAKGIEGIVNGMDIEENPKTD 289
 Db 305 NNMKAGIREADRVTVSPYAKELVSCVSGVELDNHROCGITGICNGMDTQEWNPAD 364
 QY 290 KFLSAPYDONSYYAGKAAKEALQAEGLGVPDPTAPLFAFAGRLERQKGVDIILALPKI 349
 Db 365 KYLAVKYDITITVMQAKPLKKEALQAEGLGVPDPTAPLFAFAGRLERQKGVDIILALPKI 424
 QY 350 LATPKVQIAILGTGKAAVEKLVNAIGTKYKGRAGVVKFSAPLAHLMTAGADFMVPSRF 409
 Db 425 ISM-DVQIILGTGKKEFEQTEQLEELYPKAVGVAKFNPVLAHMTAGADFMVPSRF 483
 QY 410 EPCGLIQLHAMHYGTVPVASTGGLVDTV 438
 Db 484 EPCGLIQLHAMRYGTIPICASTGGLVDTV 512

RESULT 5

Q9ZSQ5 PRELIMINARY; PRT; 607 AA.
 AC Q9ZSQ5;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Granule-bound glycogen (starch) synthase (EC 2.4.1.11).
 OS Astragalus membranaceus (Milk vetch) (Huang qi).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids I; Fabales; Fabaceae; Papilionoideae; Galegeae; Astragalus.
 OX NCBI_TaxID=83837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HAIRY ROOTS INDUCED BY RHIZOGENESIS AGROBACTERIUM LBA9402;
 RA Peng J.S., Liu D., Hu Z.B.;
 RT "cDNA cloning and structural analysis of granule-bound starch synthase
 gene of Astragalus membranaceus";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF097922; AAC70779.1; -.
 DR InterPro; IPR001296; Glycosyltransf_1.
 DR Pfam; pf00534; Glycosyltransf_1; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 607 AA; 66360 MW; 61BB0CACB94D387C CRC64;

Query Match 54.8%; Score 1254; DB 10; Length 607;
 Best Local Similarity 55.3%; Pred. No. 1.9e-87;
 Matches 250; Conservative 60; Mismatches 106; Indels 36; Gaps 9;
 QY 2 LDIYVAAEAVAPWSKTGGLGVDVGTGGLPIELVKRHRVMTIAPRYDOYADAWDTSVVVDI- 60
 Db 81 MNLVFGVGAEGVPSKGTGLGDLVGLGPPALAGNGHRVMTSPRYDQYKDAWDTGVSVEIK 140
 QY 61 MG---EKVRYPHSIKKGVRVWIDHPWFLAKVWGKTKGSKLYGPRSGADYLDNHRKRALFC 117
 Db 141 VGDIEVPFRFHSYKRGVDRVVDHPMFLKRVKWKTKGSKLYGPRSGADYLDNHRKRALFC 200
 QY 118 KAAIEAARVLPF-----GP-GEDCVFVANDHSAHPVLLKDEYQPKGQFTAKSVLA 169
 Db 201 QAALEAPRVNLNNSNYSFSGPYGEDVVFVANDHHTALLPCYLKSLYKSGIYNNKAVFC 260
 QY 170 IHNIAQGRWMEAFKDKLPQAADFCLAFSDGAKVYTEATPMEDEKPLTKGTYKKI 226
 Db 261 IHNIAQGRWMEAFKDKLPQAADFCLAFSDGAKVYTEATPMEDEKPLTKGTYKKI 300
 QY 227 KKNLWKGIIAADKLVTSPNYATEIAADAAGGVVELDTVIRAKGIEGIVNGMDIEENPKTD 286
 Db 301 KKNLWKGIIAADKLVTSPNYATEIAADAAGGVVELDTVIRAKGIEGIVNGMDIEENPKTD 360
 QY 287 KTKFLSAPYDONSYYAGKAAKEALQAEGLGVPDPTAPLFAFAGRLERQKGVDIILALPKI 346
 Db 361 QTDRIYDHYDASVTEAKAILKEALQAEGLGVPDPTAPLFAFAGRLERQKGVDIILALPKI 420
 QY 347 PKILATPKVQIAILGTGKAAVEKLVNAIGTKYKGRAGVVKFSAPLAHLMTAGADFMVPSRF 405

```
Db 421 PKFI-DQNVQIIVLGTGKIMKQIQELEVTPGKAGVAKFNSPLAHKIAGADFIVP 479
QY 407 SRPEPCGLIQLHAMHYGTVPVASTGGLVDIV 438
Db 480 SRPEPCGLIQLHAMHYGTVPVASTGGLVDIV 511

RESULT 6
Q9XIS6 PRELIMINARY; PRT; 606 AA.
AC Q9XIS6;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Granule-bound starch synthase I precursor (EC 2.4.1.21).
GN GBSSI.
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
SEQUENCE FROM N.A.
RA Isono N., Nozaki K., Ito H., Matsui H., Honma M.;
RA "Phaseolus vulgaris L. mRNA for Granule-Bound Starch Synthase I
RT (GBSSI).";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB029346; BAA82346.1; -
DR InterPro: IPR001296; Glycos_transf_1.
DR Pfam: PF00534; Glycos_transf_1; 1.
KW Glycosyltransferase; Transferase; Transit peptide.
FT TRANSIT 1 POTENTIAL.
SQ SEQUENCE 606 AA; 67080 MW; 346943F0F6DE4ADB CRC64;

Query Match 54.68; Score 1250; DB 10; Length 606;
Best Local Similarity 54.48; Pred. No. 3.8e-87;
Matches 246; Conservative 65; Mismatches 105; Indels 36; Gaps 8;

QY 2 LDIWVAEAVAPSKTGGGLGVTGGLPIELVKRGHVRMTIAPRDQYADADMTSVVVDIM 61
Db 80 MNLIFGAEVAPSKTGGGLGVTGGLPSALAEHGRVMTSPRDQYKDAWDTNVTVEVK 139
QY 62 G----EKVRFHSTKKGVHRVMDHPFLAKVWGKTSKLYGPRSGADYLDNHRFALFC 117
Db 140 VADRIETVRFHCYKQGVDRVFDHPCELEKVGKTSKLYGPRSGADYEDNQLRSLIC 199
QY 118 KAATEAARVLFP-----GP-GEDCVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA 169
Db 200 QAALFAPVRLNLSNKFSGPYGEDVIFVANDWHTALLPCYLKSNYQTRGVYRNTKVAFC 259
QY 170 IHNIAFGQRMWEAFKDTKLP---QAADFCLAFSDGYAKVYTEATPMEDEKPLTGKTY 226
Db 260 IHNISYGRPFEDFPLNLPNEYSAFD---FTDGLK-----PVRG--- 299
QY 227 KKNLWKGIIAADKLVTSVPNYATEIAADAAGVELDVTIRAKGIEGIVNGMDIEENP 286
Db 300 RKNWMAAIIESDLVLTSPYAKELVSGEDRGVLDNITRTKTVGAVGIVNGMDIREWSP 359
QY 287 KTDKFLSAPYQNSVYAGKAAKALQAEGLPVDPTAPLFAFIRGLEEQKGVDIILAAAL 346
Db 360 KTDKFDIHEDTTSVKAEKFLKALQAEGLPVNDRDIPGLGIRGLEEQKGSDDLVEAI 419
QY 347 PKILATPKVQIATLGTGAAYAKLVNATGTYKGRKGVKFSAPLAHMLTAGADFMVLP 406
Db 420 PKFI-DQNVQIILGTGKSKMEKQIEQLYPEKARGIAKFDGFLAHKIAGSDFIMP 478
QY 407 SRPEPCGLIQLHAMHYGTVPVASTGGLVDIV 438
Db 479 SRPEPCGLIQLHAMHYGTVPVASTGGLVDIV 510

RESULT 7
```

```
Q9MAQO PRELIMINARY; PRT; 610 AA.
AC Q9MAQO;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Granule-bound starch synthase.
GN F9L11.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Nguyen M., Lam B., Southwick A., Bei, Buehler E., Chin C.,
RA Chlou J., Choi E., Dunn P., Gonzalez A., Gowng B., Kim C., Koo T.,
RA Lee J.M., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsy N.,
RA Pham P., Sakano H., Schwartz J., Shinn P., Thaveri A., Toriumi M.,
RA Vaysberg M., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN EMBL: AC006424; AAF31273.1; -
DR InterPro: IPR001296; Glycos_transf_1.
DR Pfam: PF00534; Glycos_transf_1; 1.
SQ SEQUENCE 610 AA; 66879 MW; CF17F25BBL2220DF CRC64;

Query Match 54.38; Score 1242; DB 10; Length 610;
Best Local Similarity 55.38; Pred. No. 1.6e-86;
Matches 250; Conservative 59; Mismatches 107; Indels 36; Gaps 9;

QY 2 LDIWVAEAVAPSKTGGGLGVTGGLPIELVKRGHVRMTIAPRDQYADADMTSVVVDI- 60
Db 84 MSVPIGAEVGPWSKTGGGLGVTGGLPPALAAARGHVRMTICPRYDQYKDAWDTCVVQIK 143
QY 61 MGEK--VRYFHSSTKKGVHRVMDHPFLAKVWGKTSKLYGPRSGADYLDNHRFALFC 117
Db 144 VGDKVENVRFFHCYKRGVDRVFDHPITFLAKVWGKTSKLYGPRSGADYLDNHRFALFC 203
QY 118 KAATEAARVLFP-----GP-GEDCVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVLA 169
Db 204 QAALFAPVRLNLSNKFSGPYGEDVIFVANDWHTALLPCYLKSNYQTRGVYRNTKVAFC 263
QY 170 IHNIAFGQRMWEAFKDTKLP---QAADFCLAFSDGYAKVYTEATPMEDEKPLTGKTY 226
Db 264 IHNIAFGQRFADDDYSLNLPISFKSFD---FMDGYEK-----PVKG--- 303
QY 227 KKNLWKGIIAADKLVTSVPNYATEIAADAAGVELDVTIRAKGIEGIVNGMDIEENP 286
Db 304 RKNWMAAIIAHLAHLVTSVPYQAEGLISGVDGVELHKLRLMKTIVSGIINGMDVQENP 363
QY 287 KTDKFLSAPYQNSVYAGKAAKALQAEGLI PVDPTAPLFAFIRGLEEQKGVDIILAAAL 346
Db 364 STDYIDIKYDITVTDAKPLIKEALQAAVGLPVDVDPVIGFIRGLEEQKGSDDLVEAI 423
QY 347 PKILATPKVQIATLGTGAAYAKLVNATGTYKGRKGVKFSAPLAHMLTAGADFMVLP 406
Db 424 SKFMGL-NVQVILGTGKKMEQAQLELEKFPKRAVGAKFNPVLAHMITAGADFIIVP 482
QY 407 SRPEPCGLIQLHAMHYGTVPVASTGGLVDIV 438
Db 483 SRPEPCGLIQLHAMHYGTVPVASTGGLVDIV 514

RESULT 8
Q8SA49 PRELIMINARY; PRT; 603 AA.
AC Q8SA49;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Granule-bound starch synthase.
```

```

GN 259116.5.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MEREX;
RA Ma J., Samiguel P.J., Dubcovsky J., Shiloff B.A., Rostoks N.,
RA Bennett J.L.;
RA Jiang Z., Busso C.S., Klein hofs A., Devos K.M., Ramakrishna W.,
RA *Comparative sequence analysis of wx1 homologous regions in barley,
RT maize, pearl millet, rice, sorghum and diploid wheat.*;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF474373; AAL77109.1; -.
SQ SEQUENCE 603 AA; 66280 MW; 467A3D56A82125CB CRC64;

Query Match 53.9%; Score 1232.5; DB 10; Length 603;
Best Local Similarity 54.1%; Pred No. 8.1e-86;
Matches 243; Conservative 60; Mismatches 117; Indels 29; Gaps 6;

QY 2 LDIVVAAEVPWPKTGGGLDVTGGLPIELVKRHRVMTIAPRYDQYADAWDTSVVVDIM 61
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
76 MNLVFGAEMAPWSKTGGGLDVLGGLPPAMAANGHRVMVSPRYDQYKDAWTSVISEIK 135
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
62 ----GEKRYRPHSIKKGVRHWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
136 VADEYRVERVFFHCYKRGVDRVFDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 195
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
118 KAAIEARVL-----PFGP---GECVFFVANDHWSALVPVLLKDEYQPKQFTKAKSVLA 169
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
196 QAALEAPRLINNNPYFSGPVEDVFCNDWHTGLLACVLSKNSQNGIYRTAKVAPC 255
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
170 IHNTAFQGRMEEAFKDTKLQAAFDKLAFSQYAKVYTEATPMEDEKPPLTGKTKYKI 229
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
256 IHNTSYQGRFDFDQAQLNLPDRFKSSFDIDGYDK-----PVEG---RKI 298
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
230 NMLKGGIITADKLVTVSPNYATEIAADAAGGVDELDTVIRAKGIEGIVNGMDIEWPKTD 289
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
299 NWMKAGILEADRLVSPYIAELISGARGCELNDIMRLTGITGIVNGMDVSEWDPSTKD 358
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
290 KFLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFGRLEEQKGVDTIILAALPKI 349
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
359 KFLAVNYDITTALEAKALNKEALQAEGLPVDKVPVYAFVGRLEEQKGVDPVIAAIPFI 418
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
350 LATPKVQITAILGTGKAAEKLVAIGTKYKRAKGVKFSAPLAHMLTAGADFMVPSRF 409
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
419 LKEEDVQIILGTGKKKFKELLSKMEKFPKGVRAVVRFNAPLAHOMMAGADLLAVTSRF 478
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
410 EPCGLIQLHAMHYGTPVAVSTGGGLVDTV 438
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
479 EPCGLIQLGMRGTPVCACSTGGGLVDTVI 507
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3

RESULT 9
Q94LY7
ID Q94LY7 PRELIMINARY; PRT; 609 AA.
AC Q94LY7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Granule-bound starch synthase (EC 2.4.1.21).
GN WAXY.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. REXMONT;
RA Larkin P.D., McClung A.M., Ayres N.M., Park W.D.;

```

```

RT "The Wx locus (Granule Bound Starch Synthase) is strongly associated
RT with pasting curve characteristics in rice (Oryza sativa L.).";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF141954; AAF72561.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
SQ SEQUENCE 609 AA; 66466 MW; 6D2615EB203CBDC8 CRC64;

Query Match 53.7%; Score 1229; DB 10; Length 609;
Best Local Similarity 53.9%; Pred. No. 1.5e-85;
Matches 242; Conservative 61; Mismatches 116; Indels 30; Gaps 6;

QY 2 LDIVVAAEVPWPKTGGGLDVTGGLPIELVKRHRVMTIAPRYDQYADAWDTSVVVDI- 60
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
83 MNLVFGAEMAPWSKTGGGLDVLGGLPPAMAANGHRVMVSPRYDQYKDAWTSVVAEIK 142
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
61 ----MGKRYRPHSIKKGVRHWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
143 VADRYRVERVFFHCYKRGVDRVFDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 202
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
118 KAAIEARVL-----PFGP---GECVFFVANDHWSALVPVLLKDEYQPKQFTKAKSVLA 169
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
203 QAALEAPRLINNNPYFSGPVEDVFCNDWHTGLLACVLSKNSQNGIYRTAKVAPC 262
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
170 IHNTAFQGRMEEAFKDTKLQAAFDKLAFSQYAKVYTEATPMEDEKPPLTGKTKYKI 229
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
263 IHNTSYQGRFDFDQAQLNLPDRFKSSFDIDGYDK-----DTPVEG-----RKI 305
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
230 NMLKGGIITADKLVTVSPNYATEIAADAAGGVDELDTVIRAKGIEGIVNGMDIEWPKTD 289
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
306 NWMKAGILEADRLVSPYIAELISGARGCELNDIMRLTGITGIVNGMDVSEWDPSTKD 365
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
290 KFLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPLFAFGRLEEQKGVDTIILAALPKI 349
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
366 KIITAKYDITTALEAKALNKEALQAEGLPVDKVPVYAFVGRLEEQKGVDPVIAAIPFI 425
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
350 LATPKVQITAILGTGKAAEKLVAIGTKYKRAKGVKFSAPLAHMLTAGADFMVPSRF 409
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
426 M-QEDVQIILGTGKKKFKELLSKMEKFPKGVRAVVRFNAPLAHMLTAGADFMVPSRF 484
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
410 EPCGLIQLHAMHYGTPVAVSTGGGLVDTV 438
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3
485 EPCGLIQLGMRGTPVCACSTGGGLVDTV 513
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 3

RESULT 10
Q9SXX3
ID Q9SXX3 PRELIMINARY; PRT; 605 AA.
AC Q9SXX3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Starch synthase (GBSSI) (EC 2.4.1.21).
GN WAXY.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99321800; PubMed=10393240;
RT Murai J., Taira T., Ohta D.;
RT "Isolation and characterization of the three Waxy genes encoding the
RT granule-bound starch synthase in hexaploid wheat.";
RL Gene 234:71-79(1999).
DR EMBL; AB019623; BAA77351.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.

```


QY 170 IHNIAFOGRMWEAFKDTKLPQAAFDKLFASDGYAKVYTEATPMEDEKPLTGKTYKKI 229
 Db 263 IHNISYOGRAFEDYPPELNLSERFSFDFIDGY-----DTPVEG-----RKI 305
 QY 230 NWLKGGLIAADKLVTVSPNYATEIAADAAGVGLDVTIRAKGIGVINGMDIEWNPCKTD 289
 Db 306 NWMKAGILEADRVLTSPYAEELISGARCELDNIMRLTGITGIVNGMDVSEWDPKTD 365
 QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFGRLEEKQGVDDIILAALPKI 349
 Db 366 KYITAKYDATTAEAKALNEALQAEAGLPVDRKIPLIAFTIGRLEEKQGVDDVMAAIPEL 425
 QY 350 LATEPKVOIILGTGKAAEKLVAIGTKYKGRAGVVKFSPAPLAHMLTAGADFMVPSRF 409
 Db 426 M-QEDVOIILGTGKAAEKLVAIGTKYKGRAGVVKFSPAPLAHMLTAGADFMVPSRF 484
 QY 410 EPGGLIQLHAMHYGTPVWVASTGGGLVDTV 438
 Db 485 EPGGLIQLHAMHYGTPVWVASTGGGLVDTV 513

RESULT 13
 Q9SL56
 ID Q9SL56 PRELIMINARY; PRT; 604 AA.
 AC Q9SL56
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Starch synthase (GBSSI) (EC 2.4.1.21).
 GN WAXY.
 OS Triticum turgidum subsp. durum (durum wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murai J., Taira T., Ohta D.;
 RT "Isolation and characterization of the four Waxy genes encoding the
 RT granule-bound starch synthase in tetraploid wheats.";
 RL Appl. Biol. Sci. 0:0-0(1999).
 DR EMBL; AB029064; BAA88512.1; -;
 DR InterPro; IPR001296; Glycosyltransf_1.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR Pfam; PF00534; Glycosyltransf_1; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 604 AA; 66227 MW; 3509B1E28D9D9E45 CRC64;

Query Match 53.2%; Score 1217.5; DB 10; Length 604;
 Best Local Similarity 53.9%; Pred. No. 1.1e-84;
 Matches 242; Conservative 58; Mismatches 120; Indels 29; Gaps 6;
 QY 2 LDIWVAAEAPWPSKTGGLGVDVTGGLPIELVKRGRVMTIAPRYDQYADADTSSVVDIM 61
 Db 77 MNLVFGAEMAPWPSKTGGLGVDVGLGLPPAMAANGHRVMTISPRYDQYADADTSSVSEIK 136
 QY 62 ----GEKVRVFSHKGVHVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
 Db 137 VADEYERVRVPHCYKRGVDRVFDHPGCFLEKVRGKTEKIYGPAGTDYEDNQLRFSLLC 196
 QY 118 KAATEAARVL-----PF--GP-GEDCVFVANDHVSALVPVLLKDEYQPKGQFTAKSVLA 169
 Db 197 QAALAEPRILDLNNPFGPYGDEVVFCNDWHTGLLACYLKSNSYGSNGIYTAKVAF 256
 QY 170 IHNIAFOGRMWEAFKDTKLPQAAFDKLFASDGYAKVYTEATPMEDEKPLTGKTYKKI 229
 Db 257 IHNISYOGRAFEDYPPELNLSERFSFDFIDGYDK-----PVEG-----RKI 299
 QY 230 NWLKGGLIAADKLVTVSPNYATEIAADAAGVGLDVTIRAKGIGVINGMDIEWNPCKTD 289
 Db 306 NWMKAGILEADRVLTSPYAEELISGARCELDNIMRLTGITGIVNGMDVSEWDPKTD 359
 QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFGRLEEKQGVDDIILAALPKI 349
 Db 366 KYITAKYDATTAEAKALNEALQAEAGLPVDRKIPLIAFTIGRLEEKQGVDDVMAAIPEL 425
 QY 350 LATEPKVOIILGTGKAAEKLVAIGTKYKGRAGVVKFSPAPLAHMLTAGADFMVPSRF 409
 Db 426 M-QEDVOIILGTGKAAEKLVAIGTKYKGRAGVVKFSPAPLAHMLTAGADFMVPSRF 484

QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFGRLEEKQGVDDIILAALPKI 349
 Db 360 KFLAVNYDITTALEKALNEALQAEVGLPVDKRVPLVAFVIGRLEEKQGVDDVMAAIPEL 419
 QY 350 LATEPKVOIILGTGKAAEKLVAIGTKYKGRAGVVKFSPAPLAHMLTAGADFMVPSRF 409
 Db 420 LKEEDVOIILGTGKAAEKLVAIGTKYKGRAGVVKFSPAPLAHMLTAGADFMVPSRF 479
 QY 410 EPGGLIQLHAMHYGTPVWVASTGGGLVDTV 438
 Db 480 EPGGLIQLHAMHYGTPVWVASTGGGLVDTV 508

RESULT 14
 Q9SYU0
 ID Q9SYU0 PRELIMINARY; PRT; 574 AA.
 AC Q9SYU0
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Granule-bound starch synthase.
 GN WX-D1.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. WAXY;
 RX MEDLINE=99254805; PubMed=10323226;
 RA Vrinten P., Nakamura T., Yamamori M.;
 RT "Molecular characterization of waxy mutations in wheat.";
 RL Mol. Gen. Genet. 261:463-471(1999).
 DR EMBL; AF113844; AAD26156.1; -;
 DR InterPro; IPR001296; Glycosyltransf_1.
 DR InterPro; IPR000794; Ketoacyl-synt.
 DR Pfam; PF00534; Glycosyltransf_1; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 SQ SEQUENCE 574 AA; 63267 MW; 87C13579508CB402 CRC64;

Query Match 53.2%; Score 1216.5; DB 10; Length 574;
 Best Local Similarity 53.9%; Pred. No. 1.3e-84;
 Matches 242; Conservative 58; Mismatches 120; Indels 29; Gaps 6;
 QY 2 LDIWVAAEAPWPSKTGGLGVDVTGGLPIELVKRGRVMTIAPRYDQYADADTSSVVDI- 60
 Db 77 MNLVFGAEMAPWPSKTGGLGVDVGLGLPPAMAANGHRVMTISPRYDQYADADTSSVSEIK 136
 QY 61 ---MGEKVRVFSHKGVHVRWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKRALFC 117
 Db 137 VVDYERVRVPHCYKRGVDRVFDHPGCFLEKVRGKTEKIYGPAGTDYEDNQLRFSLLC 196
 QY 118 KAATEAARVL-----PF--GP-GEDCVFVANDHVSALVPVLLKDEYQPKGQFTAKSVLA 169
 Db 197 QAALAEPRILDLNNPFGPYGDEVVFCNDWHTGLLACYLKSNSYGSNGIYTAKVAF 256
 QY 170 IHNIAFOGRMWEAFKDTKLPQAAFDKLFASDGYAKVYTEATPMEDEKPLTGKTYKKI 229
 Db 257 IHNISYOGRAFEDYPPELNLSERFSFDFIDGYDK-----PVEG-----RKI 299
 QY 230 NWLKGGLIAADKLVTVSPNYATEIAADAAGVGLDVTIRAKGIGVINGMDIEWNPCKTD 289
 Db 300 NWMKAGILEADRVLTSPYAEELISGARCELDNIMRLTGITGIVNGMDVSEWDPKTD 359
 QY 290 KFLSAPYDQNSVYAGKAAAEALQAEGLPVDPTAPLFAFGRLEEKQGVDDIILAALPKI 349
 Db 360 KFLAVNYDITTALEKALNEALQAEVGLPVDKRVPLVAFVIGRLEEKQGVDDVMAAIPEL 419
 QY 350 LATEPKVOIILGTGKAAEKLVAIGTKYKGRAGVVKFSPAPLAHMLTAGADFMVPSRF 409
 Db 420 LKEEDVOIILGTGKAAEKLVAIGTKYKGRAGVVKFSPAPLAHMLTAGADFMVPSRF 479

```
QY 410 EPCGLIOLHAMHYCTVPVASTGGLVDTV 438
||||| | | | | | | | | | | | | | | | | |
Db 480 EPCGLIOLQGMRYGTPCACASTGGLVDTI 508

RESULT 15
Q9S7N5
ID 09S7N5 PRELIMINARY; PRI; 604 AA.
AC 09S7N5; 2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Starch synthase (GBSSI) (EC 2.4.1.21) (Granule-bound starch synthase
DE I).
DE WAXY OR WX-TWD OR WX-DI.
GN Triticum aestivum (Wheat), and
OS Triticum aestivum (Wheat), and
OS Aegilops tauschii (Aegilops squarrosa).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565, 37682;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=T.aestivum;
RX MEDLINE=99321800; PubMed=10393240;
RA Murai J., Taira T., Ohta D.;
RT "Isolation and characterization of the three waxy genes encoding the
RT granule-bound starch synthase in hexaploid wheat.";
RL Gene 234:71-79(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=A.squarrosa; STRAIN=CV. CPI 110799;
RA Yan L., Bhawe M., Fairclough R., Konic C., Rahman S., Appels R.;
RT "The genes encoding granule-bound starch synthases at the waxy loci of
RT the A, B and D progenitors of common wheat.";
RL Genome 0:0-0(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=T.aestivum; STRAIN=CV. CHINESE SPRING;
RX MEDLINE=20098733; PubMed=10631269;
RA Vrinten P.L., Nakamura T.;
RT "Wheat granule-bound starch synthase I and II are encoded by separate
RT genes that are expressed in different tissues.";
RL Plant Physiol. 122:255-264(2000).
DR EMBL; AB019624; BAA7352.1; -
DR EMBL; AF110375; AAF06938.1; -
DR EMBL; AF163319; AAF34135.1; -
DR InterPro; IPR001296; Glycos_transf_1.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR PROSITE; PS00606; B.KETOACYL_SYNTHASE; UNKNOWN_1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 604 AA; 66269 MW; 6F69B3AB6594AE49 CRC64;

Query Match 53.2%; Score 1216.5; DB 10; Length 604;
Best Local Similarity 53.9%; Pred. No. 1.4e-84;
Matches 242; Conservative 58; Mismatches 120; Indels 29; Gaps 6;

QY 2 LDIVVAAEAPWSKGTGLGVDTGGLPLELVKRGHRYMTAPRYDQYADAMDTSVVVDI- 60
:::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 77 MNLVFGAEAPWSKGTGLGVDTGGLGVLPMAANGHRVMTSPRYDQYADAMDTSVVSEIK 136
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 ---MGEKRVFTHSIKGVHRVWIDHPWFLAKVWGKTSKLYGPRSGADYLDNHRKFFALFC 117
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 137 VVDKVERVRYFHCYKRGVDRVFDHPCFLEKVRCKTEKIYGPDA GTDYEDNQORFSLC 196
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 118 KAAIEARVL-----PF--GP-GEDEVANDHSALVPLLKDEYQPKGQFTAKSVIA 169
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 197 QAALEVPRIILNDNNPFGSGYGEDVVFVNCNDHTGLIACYLKSNGYIYRAAKVAF 256
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 170 IHNIAFOGRMWEAEAFKDKLPQAAFDKLA FSDGYAKVYVTEATPMEDEKPPLTGKTKYKI 229
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
Db 257 IHNISYQGRFSFDDPFAQLNLPDRPKSSDFIDGYDK-----PVEG---RKI 299
QY 230 NWLKGIIAADKLVTVSPNYATEIAADAAGVGVELDTVIRAKGIEGIVNGMDIEWNPXTD 289
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 300 NWMKAGILQADKLVTVSPYAEELISGEARCELDNINRLTGTITGIVNGMDVSEWDPTKD 359
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 290 KFLSAPYDQNSVYAGKAAAKEALQAEGLPVDPTAPLFAFGRLEEQKGVDIILAAALPKI 349
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 360 KFLAVNYDITTALEGGKALNKEALQAEVGLPVDKVPVLAFIGRLEEQKGPDMIAAIPFI 419
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 350 LATPKVQITAILGTGKAAAYEKLVAIGTKYKGRAGVYKFSAPLAHMLTAGADFMVPSRF 409
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 420 LKEEDVQIVLLGTGKKKFERLLKSTEEKFPSKVRVVRFNAPLAHQMMAGADVLAITSRF 479
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 410 EPCGLIOLHAMHYCTVPVASTGGLVDTV 438
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 480 EPCGLIOLQGMRYGTPCACASTGGLVDTI 508
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: June 4, 2003, 14:56:06
Job time : 26.7603 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:49:26 ; Search time 7.79255 Seconds
(without alignments)
1653.790 Million cell updates/sec

Title: US-09-980-771A-7
Perfect score: 2288
Sequence: 1 ALDVMVAEAPWSKTGGL.....AMHYGTPVVASGGLYDTV 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued_Patents_AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1229	53.7	609	3	US-08-941-445A-7
2	1188	51.9	600	4	US-09-388-743-22
3	1185	51.8	533	3	US-08-941-445A-5
4	1164	50.9	616	4	US-09-388-743-14
5	1154	50.4	614	4	US-09-388-743-18
6	1147	50.1	615	4	US-09-388-743-2
7	870.5	38.0	641	4	US-08-836-567-10
8	862	37.7	671	4	US-09-196-390-2
9	861	37.6	649	4	US-09-192-909-2
10	859	37.5	539	3	US-08-941-445A-21
11	859	37.5	583	3	US-08-941-445A-13
12	833	36.4	801	4	US-09-388-743-26
13	826	36.1	690	4	US-09-388-743-6
14	826	36.1	767	4	US-08-836-567-8
15	817	35.7	799	4	US-09-196-390-6
16	810	35.4	698	3	US-08-941-445A-11
17	800	35.0	558	4	US-08-836-567-6
18	696	30.4	459	4	US-08-836-567-4
19	671.5	29.3	669	3	US-08-941-445A-9
20	558	24.4	477	1	US-07-735-065-2
21	558	24.4	477	1	US-08-469-202-12
22	558	24.4	477	2	US-08-484-434C-12
23	528.5	23.1	735	4	US-09-115-704-2
24	528	23.1	677	4	US-08-836-567-2
25	528	23.1	1197	4	US-08-836-567-12
26	528	23.1	1230	2	US-08-968-542C-35
27	499	21.8	533	4	US-09-388-743-10

28	471.5	20.6	1674	2	US-08-968-542C-12	Sequence 12, Appl
29	240	10.5	64	2	US-08-470-720-15	Sequence 15, Appl
30	215.5	9.4	79	2	US-08-470-720-13	Sequence 13, Appl
31	143.5	6.3	59	2	US-08-470-720-14	Sequence 14, Appl
32	129	5.6	30	2	US-08-470-720-9	Sequence 9, Appl
33	121	5.3	27	2	US-08-470-720-7	Sequence 7, Appl
34	112	4.9	34	2	US-08-470-720-11	Sequence 11, Appl
35	110.5	4.8	1037	4	US-09-134-001C-4794	Sequence 6, Appl
36	107	4.7	69	2	US-08-470-720-6	Sequence 18, Appl
37	107	4.7	111	2	US-08-470-720-18	Sequence 41, Appl
38	105.5	4.6	490	4	US-09-292-225-41	Sequence 35, Appl
39	105.5	4.6	509	4	US-09-292-225-35	Sequence 38, Appl
40	105.5	4.6	509	4	US-09-292-225-38	Sequence 1, Appl
41	100.5	4.4	387	4	US-09-457-302-1	Sequence 5024, Ap
42	99	4.3	494	4	US-09-134-001C-5024	Sequence 14, Appl
43	98	4.3	4545	2	US-08-804-227C-14	Sequence 8, Appl
44	98	4.3	4550	2	US-08-804-227C-8	Sequence 2, Appl
45	98	4.3	4550	2	US-08-804-198-2	

ALIGNMENTS

RESULT 1
US-08-941-445A-7
; Sequence 7, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941.445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-941-445A-7

Query Match 53.7%; Score 1229; DB 3; Length 609;
Best Local Similarity 53.9%; Pred. No. 3,7e-120;
Matches 242; Conservative 61; Mismatches 116; Indels 30; Gaps 6;

QY 2 LDIVMVAEAPWSKTGGLGVDTGGLPIELVKCRHRYMTAPRYDQYADAWDTSVVVDI- 60
Db 83 MNVVFVGAEMAPWSKTGGLGVDTGGLPIELVKCRHRYMTAPRYDQYADAWDTSVVVDI- 142

RESULT 7
 US-08-836-567-10
 ; Sequence 10, Application US/08836567
 ; Patent No. 6130367
 ; GENERAL INFORMATION:
 ; APPLICANT: Kossmann, Jens
 ; APPLICANT: Springer, Franziska
 ; APPLICANT: Abel, Gernot
 ; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
 ; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
 ; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FISH & NEAVE
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10020
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/836,567
 ; FILING DATE: 24-JUL-1997

```

; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04415
; FILING DATE: 09-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 41 408.0
; FILING DATE: 10-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Agrevo-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-836-567-10

Query Match 38.0%; Score 870.5; DB 4; Length 641;
Best Local Similarity 42.9%; Pred. No. 1.8e-82;
Matches 194; Conservative 80; Mismatches 139; Indels 39; Gaps 14;

QY 3 DIVVAAEAVPSKSTGSLGVTGDTGLVYKLRHVRVMTIAPRY-----DOYADAMDTIS 55
DB 132 NIIVTAAEAPYKSTGGLGDCVCSLPMALAARHVRVWVSPRYLNGSPDEKAYANAYDLD 191
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 56 V--VVDIMG--EKVRFHSIKKGVRHVRWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHK 111
DB 192 VRATVHCFGDAQEVAFVHEYRAGVDWVFDHSSYC-----RPGTP-YGDIYGA-FGDNQF 244
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 112 RFALFCKAAATEAAARVLFGP---GEDCVFVANDWHSALVPLVKDEYQPKGQFTKAKSVL 168
DB 245 RFTLLSHAACEAPLVPLGGLFTYGEKCLFLANDWHAALVPLLLAAKRYPGVYKDKARSIV 304
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 169 AIHNIAFGQRMWEAEAFKDTKLQAAAFKLAFSQYAKVYATEATPMEDEDEKPPLTGKTYKK 228
DB 305 AIHNIAHQGVPEAVTYNNLGLPPQWYGA---EWIFFTWARAALD-----TGET--- 351
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 229 INWLKGIIAADKLVTVPNYATEIADAAGGVELDIVI--RAKGIEGVNGMDIEWNP 286
DB 352 VNVLKGAIAVADRILLTYSQGSWEIIT-PEGGYGLHELLSSROSVLNGITNGIDVNDWNP 410
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 287 KTDKFLSAPDYDONSVYAKAAAEKALCAELGPLVDPTAPLFAFICGLEEOKGVDIILAAL 346
DB 411 STEHITASHYTSINDL-SGKVOCKTDLQKELGLPIRPDCPLGLFICGLDYOKGVDIILSAI 469
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 347 PKILATPKVQIAILGTCKAAEYKLVNAIGTKYKRAKGVVYKFSAPLAHMITAGADFMLVP 406
DB 470 PELMQN-DVQVVMLGSGEKQYEDMMRHTENLFKDKRAWVGFNVPVSHRITAGCDILLMP 528
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 407 SRPEPCGLIQLHAMHYGTVPVASTGGIVDTV 438
DB 529 SRFEPCLNQLYAMRYGTIPVHSTGGIRDV 560
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-09-196-390-2
; Sequence 2, Application US/09196390
; Patent No. 6307125
; GENERAL INFORMATION:
; APPLICANT: Block, Martina
; APPLICANT: Lorz, Horst
; APPLICANT: Lutticke, Stephanie
; APPLICANT: Walter, Lennart
; APPLICANT: Froberg, Claus
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
; TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH
; TITLE OF INVENTION: SYNTHESIS

```



```

Db 362 NFKGAVVADRIYVTSKYSWEVTT-AEGGGGLNELLSSRKSVLNGVINGIDINDWNP 420
QY 288 TKFLSAPYDONSAYAGKAAKEALQAEGLPVDPTAPLFAFVIGRLEEQGVDIILAALP 347
Db 421 TDKICFCHVSVDL-SGKAKCKALQKELGLPVRDVPVLGFTIGRLDYQKGDILQILIP 479
QY 348 KILATPKVQIAITLGTGKAAEYKIVNAIGTKYGRKGVVFKFSAPLAHMLTAGADFMVPS 407
Db 480 DLM-REDVQFVMLGSGDPELEDWMRSTESIFKDKRGWGVFVPSVSHRITAGCDILMPS 538
QY 408 REPCGLIQLHAMHYGTPVPVASTGGGLVDTV 438
Db 539 REPCGLNQLYAMQYGTVPVVAHTGGLRDTV 569

RESULT 10
US-08-941-445A-21
; Sequence 21, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 539 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-941-445A-21

```

```

Query Match 37.5%; Score 859; DB 3; Length 539;
Best Local Similarity 42.2%; Pred. No. 2.le-81;
Matches 190; Conservative 77; Mismatches 145; Indels 38; Gaps 12;

QY 4 IVMVAEAPWSKGTGLGVDVGGPLIELVKRGRHVTIAPRY-----DQYADAWDTSVV 57
Db 51 IVFTVGEASPYAKSGGLDVCGLPVALAARGHRVVMVMPRYLNGTSDKNYANAFYTEKH 110
QY 58 VDIM---GE-KVRFHSLKGVHVRWIDHPFLAKVWKGTSKLYGPRSGADYLDNHRF 113
Db 111 IRIPCFGGEHVTEFFHYRDSVDWVDFHESY-----HRPGLNYGDKFGA-FGDNQF 163
QY 114 ALFCKAAEAAARVLPFGP---GEDCVFVANDWHSALVPVLLKDEYQPKGQFTKAKSVIAI 170

```

```

Db 164 TLICYACEAPLILELGGYIYGQCMFVNDWHDHSLVPLVLAARYPYGVYKDSRIIVI 223
QY 171 HNIAFGQRMWEAEFKTKLPQAAFDKLAISDGVAKVYTEATPMEDEKPLITGKYKIN 230
Db 224 HNLHQGVFEASTYDPDLGLPPEWYGALEW-----VPEWARRHALDKG-----EAVN 270
QY 231 WLKGGITAAKLVTVSPNYATEIAADAAGGVELDTVI--RAKGIEGIVNGMDLEWNPKT 288
Db 271 FLKAGVAVTADRIYVTSKYSWEVTT-AEGGGGLNELLSSRKSVLNGVINGIDINDWNP 329
QY 289 DKLSAPYDONSAYAGKAAKEALQAEGLPVDPTAPLFAFVIGRLEEQGVDIILAALPK 348
Db 330 DKCIPCHYSVDL-SGRAKCKALQKELGLPVRDVPVLGFTIGRLDYQKGDILQILIP 388
QY 349 ILATPKVQIAITLGTGKAAEYKIVNAIGTKYGRKGVVFKFSAPLAHMLTAGADFMVPS 408
Db 389 LM-REDVQFVMLGSGDPELEDWMRSTESIFKDKRGWGVFVPSVSHRITAGCDILMPS 447
QY 409 FEPCGLIQLHAMHYGTPVPVASTGGGLVDTV 438
Db 448 FEPCGLNQLYAMQYGTVPVVAHTGGLRDTV 477

```

RESULT 11

```

US-08-941-445A-13
; Sequence 13, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanning
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-941-445A-13

```

```

Query Match 37.5%; Score 859; DB 3; Length 583;
Best Local Similarity 42.2%; Pred. No. 2.4e-81;
Matches 190; Conservative 77; Mismatches 145; Indels 38; Gaps 12;

QY 4 IVMVAEAPWSKGTGLGVDVGGPLIELVKRGRHVTIAPRY-----DQYADAWDTSVV 57
Db 95 IVFTVGEASPYAKSGGLDVCGLPVALAARGHRVVMVMPRYLNGTSDKNYANAFYTEKH 154

```


Sequence 8, Application US/08836567
Patent No. 6130367

GENERAL INFORMATION:

APPLICANT: Kossmann, Jens
APPLICANT: Springer, Franziska

APPLICANT: Abel, Gernot

TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES

TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC

TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,567

FILING DATE: 24-JUL-1997

CLASSIFICATION: 800

APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/04415

FILING DATE: 09-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 41 408.0

FILING DATE: 10-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: AGREVO-4

TELEPHONE: 212-596-9000

TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 767 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-836-567-8

Query Match 36.1%; Score 826; DB 4; Length 767;

Best Local Similarity 42.3%; Pred. No. 1.le-77; Mismatches 146; Indels 48; Gaps 11;

Matches 191; Conservative 67;

QY 2 LDIVMAAEVAPWSKTGGLGDTVTGGLPIELVKRGRHVMYTIAPRYDQYADAWDTSV---V 57

DB 276 MNILIVASECAPWSKTGGLGDTVTGGLPIELVKRGRHVMYTIAPRYDQYADAWDTSV---V 335

QY 58 VDMGEKRVFTSHIKKGVHRVWIDHPFLAKVNGKTGSKLYGPRSGADYLDNHRKRALFC 117

DB 336 VDGQDVEVTYFQAFIDGVDFEVID----SHMERHIGNNIY----GGRNVDILKRMVLF 386

QY 118 KAATAARVLP----FGPGEDCVFVANDHVSALVPVLLKDEYQPKGFTKAKSVLAHN 172

DB 387 KAALFVPHVPCGVGVGSGDGLNLFVIANWHVLLPVILKAYIRDNNGIMNTRSVLVHN 445

QY 173 IAFQRMWEAFKDKLPFAAFDKLAFSDGYAKVYVTEATPMEDEKPLTKYKKNWL 232

DB 446 IAHQGRGPLEDFSVDLPVPPHMDPFKLYD-----PVGGEHF---NIF 484

QY 233 KGLIADKLVTVSPNTATEIADAAGGVLDIVIRAKG--IEGIVNGMDIEEWNPKTDK 290

DB 485 AAGLKTADRVVTVSHGYSWEIKT--SQGGWGLHQIINENDMKIQIVNGIDTKWNPEDLV 543

QY 291 FLAP-----YDONSIVAGKAAAKALQALGLPVDPTAPLFAFTGRLEEQKGVDIILAAL 346

DB 544 HLQSDGYMNYSLDTLQTKPKQCKAAALOKELGLPVRDDVPLIGFTIGRDPKQGVDLIAEAS 603

QY 347 PKILATPKVOITAILGTGKAAYEKIVNAIGTKYKGRAGVYVVKFSAPLAHMLTAGADEMLVP 406

DB 604 AMMG-QDVQLVGLTGTGRDLQMLRQFECQHNDKIRGWGVSFKTSHRITAGADILLMP 662

QY 407 SREPCGLIQLHAMHYGTVPVAVSTGGGLVDTV 438

DB 663 SREPCGLNQLYAMKYGTIPVHAVGGIRDTV 694

RESULT 15

US-09-196-390-6

Sequence 6, Application US/09196390

Patent No. 6307125

GENERAL INFORMATION:

APPLICANT: Block, Martina

APPLICANT: Lorz, Horst

APPLICANT: Lutticke, Stephanie

APPLICANT: Walter, Lennart

APPLICANT: Froberg, Claus

APPLICANT: Kossmann, Jens

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES

TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH

TITLE OF INVENTION: SYNTHESIS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/196,390

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 196 21 588.9

FILING DATE: 29-MAY-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 196 36 917.7

FILING DATE: 11-SEP-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP97/02793

FILING DATE: 28-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Haley, Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: AGREVO-9

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 799 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-196-390-6

Query Match 35.7%; Score 817; DB 4; Length 799;

Best Local Similarity 41.8%; Pred. No. 1.le-76;

Matches 190; Conservative 67; Mismatches 144; Indels 54; Gaps 12;

QY 2 LDIVMAAEVAPWSKTGGLGDTVTGGLPIELVKRGRHVMYTIAPRYDQYADAWDTSV--VVD 59

DB 308 MNVVAECSPCKTGTGLGDTVTGGLGDTVTGGLGDTVTGGLGDTVTGGLGDTVTGGLGDTVT 367

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:56:21 ; Search time 13.5267 Seconds
(without alignments)
3342.965 Million cell updates/sec

Title: US-09-980-771A-7
 Perfect score: 2288
 Sequence: 1 ALDIYVMAAEVAPWSKTGGL.....AMHYGTVPWASTGGIVDTV 438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp:*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pcp:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp:*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pcp:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pcp:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	1267	55.4	636	9	US-10-138-075-4	Sequence 4, Appli
2	1247.5	54.5	609	9	US-10-138-075-2	Sequence 2, Appli
3	1211.5	53.0	599	9	US-10-138-075-5	Sequence 5, Appli
4	862	37.7	671	10	US-09-952-677-2	Sequence 2, Appl
5	817	35.7	799	10	US-09-952-677-6	Sequence 6, Appl
6	528.5	23.1	909	9	US-10-163-214-2	Sequence 2, Appli
7	513.5	22.4	915	9	US-10-163-214-6	Sequence 6, Appli
8	511.5	22.4	874	9	US-10-163-214-13	Sequence 13, Appl
9	511.5	22.4	914	9	US-10-163-214-12	Sequence 12, Appl
10	387	16.9	474	12	US-10-007-693-99	Sequence 99, App
11	383.5	16.8	476	12	US-10-007-693-69	Sequence 69, App
12	348	15.2	293	9	US-10-163-214-10	Sequence 10, Appl
13	215.5	9.4	117	10	US-09-739-438-2	Sequence 2, Appl
14	176.5	7.7	409	9	US-09-738-626-4738	Sequence 4738, Ap
15	164	7.2	143	10	US-09-739-438-4	Sequence 4, Appl
16	156	6.8	381	9	US-09-738-626-5896	Sequence 5896, Ap
17	126	5.5	191	10	US-09-924-358-22	Sequence 22, App
18	122.5	5.4	418	9	US-09-738-626-3951	Sequence 3951, Ap
19	110.5	4.8	421	9	US-10-163-214-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-138-075-4

: Sequence 4, Application US/10138075

; Publication No. US20030087369A1

GENERAL INFORMATION:

APPLICANT: Broglie, Karen E.

APPLICANT: BUTLER, Karlene H.

APPLICANT: HARVEY LESLIE T. BULLER, KATHLENE H.

APPLICANT: HAIVELL, LESLIE T.
APPLICANT: Lightner, Jonathan F

APPLICANT: LIGNIER, JONAS
APPLICANT: OROSCO, EMIL M

APPLICANT: UOZCO, EMIL M.

; TITLE OF INVENTION: GRANU-
 : FINE PREFERENCE: PP1474 NA

FILE REFERENCE: BBI4/4 NA
CURRENT APPLICATION NUMBER: HS/10/128 075

; CURRENT APPLICATION NUMBER: US/103
: CURRENT FILING DATE: 2002-05-02

1 ; CURRENT FILING DATE: 2002-05-02
2 ; PRIOR PUBLICATION NUMBERS: 600398 315

;; PRIOR APPLICATION NUMBER: 60/

; PRIOR FILING DATE: 2001-05-03

; NUMBER OF SE

; SOFTWARE: MI

; SEQ ID NO 4

; LENGTH: 636

```

; TYPE: PRT

```

Query Match 55.4%; Score 1267; DB 9; Length 636;
Best Local Similarity 55.4%; Pred. No. 1e-102;
Matches 251; Conservative 55; Mismatches 113; Indels 34; Gaps 7;

QY

2 LDIWAAEVA^{PWSKTGSLGLDVTCGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVV}D I - 60
:
:

DZ	100	MIFIIIGIEVAFWCAIUGSLDVJLGGLPFPALAGFGRHVMTIVKRIQIDANDJTSVMIEVK
QY	61	---MGEKVRETHSIKKGVHRVTWDHPWFIAKWVGKTGSKLKPSRGADYLDNHRKFALFC

Db 166 VGDTEKVRPFHCYKRGVDRVFVDHPWFLEKVGWGTGQKLYGPTTGNDEYDNLQRFSLFC 225

226 QAALEAPRVLSNSSKVSFGPYGEDVIFVANDWHHTLIPCYLJKSMYOSRGYYNARVVC 285

Db 286 IHNIAVQGRFAFAADFSLLNLPDQKSSFDFFIDGHVK-----PVVG---RKI 328

QY 230 NWLKGIIAADKLVTVSPNYATEIAADAAGVELDTVIRA-----KGTEGVNGMDIEWN 285

Db 329 NWLKGIIIESFWITVSPNKAELVSGDKGVLDNIRKIDDDRLVGVNGMDVQEW 388

QY 286 PKTDKFLSAPYDQNSVYAGKAAKEALQAEGLGVPDPTAPLFAFVIGRLEEGKGVDTILAA 345

Db 389 PTDKYLAVKYDVSTVLEAKALLKEALQAEVGLPVDNRNIPLIGRLEEGKGVDTILAA 448

QY 346 LPKLILATPKVOJAILGTGKAAEYKLVNAIGTKYGRAGVVKFSAPLAHMLTAGADFWLV 405

Db 449 IPOET-KONVOLVALGTGKKOMEKOLELEISYDPKARGVAKFNVPPLAHMLTAGADFLV 507

QY 406 PSREPCGLIOLHAMHYGTVPVASTGGLVDV 438

Db 508 PSREPCGLIOLQAMRYGSPVIVASTGGLVDV 540

RESULT 2

US-10-138-075-2

; Sequence 2, Application US/10138075

; Publication No. US20030087369A1

; GENERAL INFORMATION:

; APPLICANT: Broglie, Karen E.

; APPLICANT: Butler, Karlene H.

; APPLICANT: Harvell, Leslie T.

; APPLICANT: Lightner, Jonathan E.

; APPLICANT: Orozco, Emil M.

; TITLE OF INVENTION: Granule-Bound Starch Synthase

; FILE REFERENCE: BB1474 NA

; CURRENT APPLICATION NUMBER: US/10/138,075

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 60/288,315

; PRIOR FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 2

; LENGTH: 609

; TYPE: PRT

; ORGANISM: Zea mays

US-10-138-075-2

Query Match 54.5%; Score 1247.5; DB 9; Length 609;

Best Local Similarity 54.7%; Pred. No. 5e-101;

Matches 246; Conservative 60; Mismatches 113; Indels 31; Gaps 8;

QY 2 LDIWVAEAVAPWSKTTGGLGDTGGLPIELVKGHRVMTIAPRYDOYADANDTSVVDI- 60

Db 81 MTIVFVATEVHPWCKTGGLGDPVGLPPALAAAGHRVMTIAPRYDOYKDWDTSVLVEVN 140

QY 61 MG---EKVRYFHSIKKGVRVWIDHPWFLAKVWCKTGSGLYKPRSGADYLDNHRKRFALFC 117

Db 141 IGDVVEIVRFHCYKRGVDRVFDHPMELEKWKGTGAKLYGPTGIDYRDNQLRFLC 200

QY 118 KAAIEARVLPF-----GP-GEDEVFVANDHWSALVPLVLLKDYQPKGQFTKAKSVLA 169

Db 201 LAALAPRVLNFNNSYFSGPYGEDVVFVANDHWTAILPCYLKSMYKNGYKNAKVAFC 260

QY 170 IHNIAFOGRMWEAEAFKDKLPQAAFDKLAFLSDGAKVYVTEATPMEDEKPLTGKTKYKI 229

Db 261 IHNIAVQGRFARADFDLNLNPSDFDFFIDGHVK-----PVVG---RKL 303

QY 230 NWLKGIIAADKLVTVSPNYATEIAADAAGVELDTVIRA-----KGTEGVNGMDIEWNPKT 288

Db 304 NWMKAGIIESDLVTVSPHYVKELTSGDKGVLDGLVLRTPLEIGVINGMDVYEDWDPST 363

QY 289 DKFLSAPYDQNSVYAGKAAKEALQAEGLGVPDPTAPLFAFVIGRLEEGKGVDTILAA 348

Db 364 DKYISAKYDADTATVTEARLNKRLQAEVGLPVDSSIPVIVFVGRLEEGKGVDTILAA 423

QY 349 ILATPKVOJAILGTGKAAEYKLVNAIGTKYGRAGVVKFSAPLAHMLTAGADFWLVPSR 408

Db 424 FVG-ENVQIIVLGTGKKKMEELTQLEVYNNARGIAKFNVPPLAHMMFAGADFIIVPSR 482

QY 409 FEPGGLIOLHAMHYGTVPVASTGGLVDV 438

Db 483 FEPGGLIOLQMGRYGVIPICSSSTGGLVDV 512

RESULT 3

US-10-138-075-5

; Sequence 5, Application US/10138075

; Publication No. US20030087369A1

; GENERAL INFORMATION:

; APPLICANT: Broglie, Karen E.

; APPLICANT: Butler, Karlene H.

; APPLICANT: Harvell, Leslie T.

; APPLICANT: Lightner, Jonathan E.

; APPLICANT: Orozco, Emil M.

; TITLE OF INVENTION: Granule-Bound Starch Synthase

; FILE REFERENCE: BB1474 NA

; CURRENT APPLICATION NUMBER: US/10/138,075

; CURRENT FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: 60/288,315

; PRIOR FILING DATE: 2001-05-03

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 5

; LENGTH: 599

; TYPE: PRT

; ORGANISM: Triticum aestivum

US-10-138-075-5

Query Match 53.0%; Score 1211.5; DB 9; Length 599;

Best Local Similarity 53.1%; Pred. No. 7e-98;

Matches 239; Conservative 63; Mismatches 117; Indels 31; Gaps 7;

QY 2 LDIWVAEAVAPWSKTTGGLGDTGGLPIELVKGHRVMTIAPRYDOYADANDTSVVDIM 61

Db 72 MPIIFVATEVHPWCKTGGLGDPVGLPPALAAAGHRVMTIAPRYDOYKDWDTNVLVEVI 131

QY 62 ---GEKRYFHSIKKGVRVWIDHPWFLAKVWCKTGSGLYKPRSGADYLDNHRKRFALFC 117

Db 132 VDRTEIVRFHCYKRGVDRVFDHPMELEKWKGTGSKLYGPTGIDYRDNQLRFLC 191

QY 118 KAAIEARVLPF-----GP-GEDEVFVANDHWSALVPLVLLKDYQPKGQFTKAKSVLA 169

Db 192 LAALAPRVLNFNNSYFSGPYGENVWFVANEWHTAVLPCYLKSMYKNGYKNAKVAFC 251

QY 170 IHNIAFOGRMWEAEAFKDKLPQAAFDKLAFLSDGAKVYVTEATPMEDEKPLTGKTKYKI 229

Db 252 IHNIAVQGRFPRVDFEELNLPESFMPSPDFVGLGHVK-----PVVG---RKI 294

QY 230 NWLKGIIAADKLVTVSPNYATEIAADAAGVELDTVIRA-----KGTEGVNGMDIEWNPKT 288

Db 295 NWMKAGITECDVLTVSPHYVKELTSGPEKGVLDGLVLRTPLEIGVINGMDVYEDWDPST 354

QY 289 DKFLSAPYDQNSVYAGKAAKEALQAEGLGVPDPTAPLFAFVIGRLEEGKGVDTILAA 348

Db 355 DKYISVKYNATVTEARLNKRLQAEVGLPVDSSIPVIVFVGRLEEGKGVDTILAA 414

QY 349 ILATPKVOJAILGTGKAAEYKLVNAIGTKYGRAGVVKFSAPLAHMLTAGADFWLVPSR 408

Db 415 FL-ENVQIIVLGTGKKKMEELTQLEVYNNARGIAKFNVPPLAHMMFAGADFIIVPSR 473

QY 409 FEPGGLIOLHAMHYGTVPVASTGGLVDV 438

Db 474 FEPGGLIOLQMGRYGVIPICSSSTGGLVDV 503

RESULT 4

US-09-952-677-2

; Sequence 2, Application US/09952677

; Patent No. US20020138876A1

; GENERAL INFORMATION:

Query Match 35.7%; Score 817; DB 10; Length 799;
Best Local Similarity 41.8%; Pred. No. 4.3e-63;
Matches 190; Conservative 67; Mismatches 144; Indels 54; Gaps 12;


```
Query Match 16.9%; Score 387; DB 12; Length 474;
Best Local Similarity 28.6%; Pred. No. 1.1e-25;
Matches 134; Conservative 63; Mismatches 182; Indels 90; Gaps 18;

QY 2 LDIVMAAEVAPWSKGGGLDVTGGPIELVKKGRHVMTIAPRYDQVADAWDSVVDIM 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MKIHTAIEFAPVKAAGGLDGLYGL-AKALAAHHTTEVVIPYKFLTFLPKEODLCSI- 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 GEKRYE-----HSIKGVHRVWIDHPWFLAKVWGKSGKLYGPRSGADYL 107
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 -OKLSYFFAGEQEATAESFYEGIKVTLFKL-----DIOPELFENAEITYS 104
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 108 DNHRKRALFCKAAI-----FAARVLPFGGDCVFFVANDWHSALVPVLLKDEYQPKGQFT 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 105 DDAFRFCFASAAAASYIOKEGANIVHL-----HDWHTGLVAGLLKQ-QPCSQLQ 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 163 KAKSVLAHNIAPQGRWEEAFKDTKLPOAFDKLAFSDGYAKYVTEATPMEDEKPLT 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 153 KI--VLTNHFVGYRGTTRILEASSLNE-----FYISQYQLFRDPQTCVL 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 223 GKYKKNLWKGGLIAADKLVTPSPNYATEIAADAAGVVELDTVIRAK--GIEGVNGMD 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 197 -----LKGALYCSDFVTTSPTYAKELLEDYS-DYELHDAITARQHHLGILNGID 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 IEWNPKTDKFLSAPYDQ-----NSVYAGKAAAKEALQAEGLPVPDPTAPLFAFIRGLE 334
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 TTWGPETDPLAKNYTKELFETPSIFFEAKAENKALYERLGLSLE-HSPVCVCIISRIA 305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 335 EOKGVDDILALPKILATPKVQJAILGT--GKAAYEKLNV--AIGIKYKGRAGVVKFS 389
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 EQGPHPMKQAILHALENAVYTLI-IIGTCYGNQHEEFANQESLANSDDVRI--LTIYS 362
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 390 APLAHLMTAGADEMLVPSRFPGLIQLHAMHYGTPVVAAGVSTGGLVDTV 438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 DVLARQIFAADMICIFSMEEPCGLTQMIGRYGTVPVLRATGGLADTV 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-007-693-69
; Sequence 69, Application US/10007693
; Patent No. US20020146776A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.515C2
; CURRENT APPLICATION NUMBER: US/10/007.693
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 69
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-007-693-69

Query Match 16.8%; Score 383.5; DB 12; Length 476;
Best Local Similarity 29.3%; Pred. No. 2.2e-25;
Matches 138; Conservative 62; Mismatches 172; Indels 99; Gaps 21;

QY 4 IWVMAAEVAPWSKGGGLDVTGGPIELVKKGRHVMTIAPRYDQVADAWDSVVDI 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 IVQVAVEFTPIVKGVLGDVAVASLAKELAKO-NDVEVLLPHYLPLSKFSS-----QV 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 MGEKRYEHSIKGVHRVWIDHPWFLAKVWGKSGKLYGP-----RSGAD 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 LSERSFYE-----FLGQQASALSYSEGLTLITITLDSQIELEFSTISV 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 106 YLDNH-KRFALFCKAAIEARVLPFGGDCVFFVANDWHSALVPVLLKDEYQPKGQFTKA 164
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 YSENNVRFSAFAAAA--AAVQLQADPAD--IVHLHDWVHVGLLAGLLKNPLNP-----VHS 151
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 165 KSVLAHNIAPQGRWEEAFKDTKLPOAFDKLAFSDGYAKYVTEATPMEDEKPLTCK 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Query Match 15.2%; Score 348; DB 9; Length 293;
Best Local Similarity 37.1%; Pred. No. 1.4e-22;
Matches 82; Conservative 44; Mismatches 77; Indels 18; Gaps 5;

QY 228 KINWLKGGIIAADKLVTPSPNYATEIAADAAGVVELDTVIRAKGIEGVNGMDIEWNPK 287
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 RINAVGAVVYSNIVTIVSPYALEVRSEGGGLQDTLVKHSRKKFLGILNGIDTDTWNP 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 288 TDKELSAFYDQNSVYAGKAAAKEALQAEGL-PVDPPTAPLFAFIRGLEQKGVDDILAL 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TDRLYKLVQYNKDL-QGKAANKAALREQLNLASAYPSQPLVGCITRLVAQKGVHLIRHAI 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 347 PKILATPKVQJAILGTGKAAYEKLNVATGTYKGR-----KGVVKSAPLAHMT 397
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 YK-TAELGGQFVLLGSSP-----VPEIQREFEGADHFNQNNNRLILIKYDDALSHCIY 172
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 398 AGADFMVPSRFPGLIQLHAMHYGTPVVAAGVSTGGLVDTV 438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 RASDMFIVPSIFEPGCLTQMIAIRYGVPIVEKGTGLNDSV 213
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-739-438-2
; Sequence 2, Application US/09739438
; Patent No. US2002029394A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Thorpe, Cathy
; TITLE OF INVENTION: Homologs of Starch Synthase D01
```

```

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/739,438
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/171514
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-739-438-2

Query Match
Best Local Similarity 9.4%; Score 215.5; DB 10; Length 117;
Matches 41; Conservative 17; Mismatches 25; Indels 5; Gaps 1;

QY 356 QAILGTG-----KAAEKLVAIGTKYKGRAGWKFSAPLAHLMTAGADFMVPSRFE 410
Db 8 QVLLGSAPDHRIGQDFTNLASKLHGEVHGRVKLCIYDEPLSHLIYAGADFIIVPSMFE 67

QY 411 PCGLIQHMHYGVPPVASTGGGLVDIV 438
Db 68 PCGLTQLTAMRYGSIPIVRKTGGGLVDIV 95

```

```

RESULT 14
US-09-738-626-4738
; Sequence 4738, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4738
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4738

```

```

Query Match
Best Local Similarity 7.7%; Score 176.5; DB 9; Length 409;
Matches 66; Conservative 37; Mismatches 99; Indels 37; Gaps 11;

QY 210 ATPMEDE--KPLTGTGTYKKNWL-KGGIIAADKLVTSPNYATEIAADAGGVLDIV 266
Db 129 AHSLDPKRWKQLGGYDVSSEKNAMEYADAVIAYSARKKDSILA-AYPIEPDNV 187

QY 267 IRAKIEGIVNGMDIEENPKTKFLSAPYDQNSVYAGKAAKEALQAEGLPVDPTAPL 326
Db 188 -----RVVLNGIDTQLWQPR-----PTFDD-----AEDSVLRSLG--VDPQPI 224

QY 327 FAFGRLEQKGVDDIILALPKILATPKVOIAILGTGKAAEY--KLVNAIGTKYKGRAGK 384

```

```

Db 225 VAFVGRITRQKGVHEHLIKA--AALEDESQVLVLCAGADPTPEIAARTTALVEELOAKREG 282
QY 385 VVKFSAPLA-----HMLTAGADFMVPSRFEPCGLIQHMHYGVPPVASTGGGLVDIV 438
Db 283 IFWQDMLGKDKIQEILTA-ADTFVCPYSIYELGIVNLEAMACNTAVASDVGGIPEVV 340

RESULT 15
US-09-739-438-4
; Sequence 4, Application US/09739438
; Patent No. US20020029394A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Thorpe, Cathy
; TITLE OF INVENTION: Homologs of Starch Synthase DUI
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/739,438
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/171514
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (104)
; NAME/KEY: UNSURE
; LOCATION: (136)
US-09-739-438-4

```

```

Query Match
Best Local Similarity 7.2%; Score 164; DB 10; Length 143;
Matches 49; Conservative 23; Mismatches 71; Indels 62; Gaps 5;

QY 106 YLDNHRKRFALFCKAAIEAARVLPFGGDCVFEVANDHISALVPVLLKDEYQPKGQFTKAK 165
Db 1 YSNDESREFGFCHSALEFLRQNGSSPD---LIHCHDSSAPVWLFKEQYAQNG-LSNGR 56

QY 166 SVLAHNIATCGRMWEEAFKDKLPQAAFDKLPFSDGYAKYITEATPMEDEKPPLAGKT 225
Db 57 VFTIHNLEFCAHH-----IGKA 74

QY 226 YKKNLWLGGLIADKLVTSPNYATEIAADAGGVLDIVIRAKGIEGIVNGMDIEEN 285
Db 75 MAR-----CDKATTVTYTSREVSGHGATAPHFSX-----FHGIRNGIDPDID 118

QY 286 PKTDKFLSAPYDQNSVYAGKAAAKE 310
Db 119 PYSDFIPVHYTSENVVYXGKSAARK 143

```

Search completed: June 4, 2003, 15:15:32
Job time : 20.5267 secs

This Page Blank (uspto)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 08:28:25 ; Search time 2768.82 Seconds
(without alignments)
16743.883 Million cell updates/sec

Title: US-09-980-771A-8

Perfect score: 1593

Sequence: 1 gcgttgacatcgtgatgtt.....ccgttgccgagaagatcccc 1593

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1593	100.0	1593	6	AX049329	Sequence
2	1593	100.0	1953	6	AX049325	Sequence
3	1593	100.0	2124	6	AX049323	Sequence
4	1593	100.0	3117	6	AX049322	Sequence
5	1591.4	99.9	3240	8	AF026420	Chlamydom
6	1314	82.5	1314	6	AX049327	Sequence
7	603.8	37.9	5856	8	AF433156	Chlamydom
8	535.8	33.6	2289	8	AF286320	Triticum v
9	530	33.3	1812	8	AF486514	Hordeum v
10	530	33.3	2311	8	HVWAXYR	Hordeum v
11	528.4	33.2	1827	8	AF486515	Barley mRNA
12	528.4	33.2	1827	8	AF486518	Hordeum v
13	525.2	33.0	1812	8	AF486519	Hordeum v
14	525.2	33.0	1827	8	AF486516	Hordeum v
15	525.2	33.0	1827	8	AF486517	Hordeum v
16	524.6	32.9	2127	8	AF163319	Triticum
17	523	32.8	1605	8	AF250137	Triticum
18	505.4	31.7	2028	8	AF113844	Triticum
19	505.2	31.7	2186	8	TAWAXYSS	Triticum
20	505.2	31.7	2267	8	AY050174	Wheat waxy
21	481.4	30.2	1801	8	AF113843	Triticum
22	474.8	29.8	2267	6	AR195560	Triticum
23	472.8	29.7	2115	8	AB089141	Sequence
24	453.2	28.4	2287	8	SB023945	Setaria i
25	449	28.2	1937	8	AB066093	Sorghum bic
26	449	28.2	1937	8	AB066094	Oryza sat
27	447.4	28.1	2542	6	AR106491	Oryza sat
28	447.4	28.1	2542	8	OSWX	Sequence
29	347	21.8	2168	8	MEGBSS	O.sativa Wa
30	340.2	21.4	2270	8	AF210699	M.esculenta
31	329.6	20.7	2221	8	AB029546	Perilla f
32	321.6	20.2	2211	8	AB071604	Phaseolus
33	316.8	19.9	2161	6	AX394246	Ipomoea b
34	313.2	19.7	2345	8	AMA6293	Sequence
35	312.8	19.6	3049	8	AF026421	Antirrhin
36	305.6	19.2	2124	8	IBU4126	Chlamydom
37	298	18.7	2092	8	AY094405	Ipomoea bat
38	298	18.7	2115	8	AY088544	Arabidops
39	298	18.7	2192	8	AY123983	Arabidops
40	289.6	18.2	2107	8	AF097922	Arabidops
41	283.2	17.8	764	8	AF446083	Astragalu
42	279.6	17.6	2035	8	PSSTARSYN	Miscanthu
43	274.2	17.2	2081	8	AF109395	P.sativum m
44	274	17.2	764	8	AF446082	Triticum
45	273.2	17.2	721	8	AF446081	Microsteg
						AF446081 Cleistach

ALIGNMENTS

RESULT 1	AX049329	AX049329	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
LOCUS	AX049329	AX049329	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
DEFINITION	AX049329	AX049329	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
ACCESSION	AX049329	AX049329	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
VERSION	AX049329.1	AX049329.1	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
KEYWORDS	AX049329.1	AX049329.1	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
SOURCE	AX049329.1	AX049329.1	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
ORGANISM	AX049329.1	AX049329.1	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
REFERENCE	AX049329.1	AX049329.1	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
AUTHORS	AX049329.1	AX049329.1	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
TITLE	AX049329.1	AX049329.1	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001
JOURNAL	AX049329.1	AX049329.1	Sequence 8	from Patent WO0071734.	1593 bp	DNA	linear	PAT 12-JAN-2001

Pred. No. is the number of results predicted by chance to have a

```

CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
  Location/Qualifiers
    1..1593
      /organism="synthetic construct"
      /db_xref="taxon:32630"
      /note="fragment de l'ADN complet codant la GBSSI de
      Chlamydomonas reinhardtii"
      <1..>1593
    CDS
      /note="unnamed protein product"
      /codon_start=1
      /transl_table=11
      /protein_id="CAC21783.1"
      /db_xref="GI:12226097"
      /translation="ALDIDVMAAEVAPWSKTLGGLDVTGGLPFIELVRRHVRMTIAPR
      YDOVADWDTSVVVDIMGEKVRYPHSIKGVHRVIMIDHPWELAKWVKTKGSKLYGPRS
      GADYLDNKEKFAKCAIEAARVLPFGEDDCVFVANDHESALVPLLKDEYOPKGO
      FTKAKSVLAHTNIAFOGRMEEAFKDKLQAADFKAFLSDGYAKYVTEAPFMEDEK
      PPLGKTKIKLWUGGLIADKLVTSPNTATEADAAGVVELDVIIRAKLEGIV
      NGMDIEMNPKTDFLSAPYDONSVYAGAAKAEALQAEGLPDPYAPLFAFIEGRLE
      EQGVDIILALPKILATPKYQIAILGTGKAAEYKLNAGIKTKYGRKAGVYKFSAPL
      AHMLTGADFMVPSRFEPGGLIOLHAMHYTPVAVASTGGGLVTVKRGVTFHMGAL
      NPDKLDEADALAAATVRRASEVFAGGRYPBMWANCISQDLWSKPAQKWEGLLEEVV
      YGKGVATAKKEELKVPVAKIP"
      290 a 539 c 510 g 254 t
BASE COUNT
ORIGIN
  Query Match 100.0%; Score 1593; DB 6; Length 1593;
  Best Local Similarity 100.0%; Pred. No. 2.4e-166;
  Matches 1593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCTGGACATCGTATGGTTGCTGCTGAGGTGCGCCCTTGGTCCAAAGCGGGCGGCGTG 60
Db 1 GCGCTGGACATCGTATGGTTGCTGCTGAGGTGCGCCCTTGGTCCAAAGCGGGCGGCGTG 60
QY 61 GCGATGTGACTGGTGGCTGCTATTGAGCTGGTCAAGCGGGCACCGCGCTCATGACC 120
Db 61 GCGATGTGACTGGTGGCTGCTATTGAGCTGGTCAAGCGGGCACCGCGCTCATGACC 120
QY 121 ATTGCCCTCGCTAGCAGCAGTACGCTGACGCTGGGACACCTCGGTGGTGGTGGACATC 180
Db 121 ATTGCCCTCGCTAGCAGCAGTACGCTGAGCGCTGGGACACCTCGGTGGTGGTGGACATC 180
QY 181 ATGGGGGAGAGGTGCGTACTTCCACTCCATCAAGAGGGGCTGCACCGGTGTGGATT 240
Db 181 ATGGGGGAGAGGTGCGTACTTCCACTCCATCAAGAGGGGCTGCACCGGTGTGGATT 240
QY 241 GACCACCCCTGTTCTTGSCCAAGTCTCTGGGCAAGACCGGCTCCAAAGCTGTACGGCCGC 300
Db 241 GACCACCCCTGTTCTTGSCCAAGTCTCTGGGCAAGACCGGCTCCAAAGCTGTACGGCCGC 300
QY 301 CGCTCCGGCGCTGACTACTTGACACCAACCAAGCGCTTCGCCCTGTCTCTGTCGAGGCAAC 420
Db 301 CGCTCCGGCGCTGACTACTTGACACCAACCAAGCGCTTCGCCCTGTCTCTGTCGAGGCAAC 420
QY 361 ATTGAGGTGCGCGGTGCTGCTGCTGCGCCCGGGGAGGACTGCTCTCTGTCGAGGCAAC 480
Db 361 ATTGAGGTGCGCGGTGCTGCTGCTGCGCCCGGGGAGGACTGCTCTCTGTCGAGGCAAC 480
QY 421 GACTGGCACTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 GACTGGCACTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 TTCACAAAGGCAAGTGGTGGTGTATCCACACATCGCTTCCAGGGCGGCGCATGTGG 540
Db 481 TTCACAAAGGCAAGTGGTGGTGTATCCACACATCGCTTCCAGGGCGGCGCATGTGG 540
QY 541 GAGGAGGCTTTCAGGACACGAGTGCCTCCAGGGCGGCGCTTTCACAGCTGGCTTCTCG 600
Db 541 GAGGAGGCTTTCAGGACACGAGTGCCTCCAGGGCGGCGCTTTCACAGCTGGCTTCTCG 600
QY 601 GAGCGGTATGCCAAGGTTTACACTGAGGCGCACCCCATGAGGAGGACGAGAGCCCGCCG 660
Db 601 GAGCGGTATGCCAAGGTTTACACTGAGGCGCACCCCATGAGGAGGACGAGAGCCCGCCG 660
```

```

QY 661 CTGACGGGAAGACCTACAAGAAGATCAACTGGCTGAAGGGTGGCATTTATCCGCCCGGAC 720
Db 661 CTGACGGGAAGACCTACAAGAAGATCAACTGGCTGAAGGGTGGCATTTATCCGCCCGGAC 720
QY 721 AAGCTGGTACTGTGTGCGCCAACTACGCGACCGAGATCGTCCGATGCCCGCGCGGT 780
Db 721 AAGCTGGTACTGTGTGCGCCAACTACGCGACCGAGATCGTCCGATGCCCGCGCGGT 780
QY 781 GTGAGCTGGACACCGTCAATCGCGCAAGGCATTGAGGGCATTTGTAACGGCATGGAC 840
Db 781 GTGAGCTGGACACCGTCAATCGCGCAAGGCATTGAGGGCATTTGTAACGGCATGGAC 840
QY 841 ATTGAGGAGTGGAAACCCCAAGACCGACAAAGTTCCTGTCTGTGCGCCCTACGACCAACAC 900
Db 841 ATTGAGGAGTGGAAACCCCAAGACCGACAAAGTTCCTGTCTGTGCGCCCTACGACCAACAC 900
QY 901 GTCTAGCGGGCAAGGCGCCGCCCAAGGAGGAGCGCTTCAGGCGAGCTGGCGCTGCTGTG 960
Db 901 GTCTAGCGGGCAAGGCGCCGCCCAAGGAGGAGCGCTTCAGGCGAGCTGGCGCTGCTGTG 960
QY 961 GACCCACCGCGCCCGCTTTCATCGCGCGCTTCATCGCGCGCTTCATCGCGCGCTTCATCGCG 1020
Db 961 GACCCACCGCGCCCGCTTTCATCGCGCGCTTCATCGCGCGCTTCATCGCGCGCTTCATCGCG 1020
QY 1021 ATCATCTGGCGCGCTTCGCGCAAGATTCCTGCGCACCCCAAGGTGAGATCGCCATCCTG 1080
Db 1021 ATCATCTGGCGCGCTTCGCGCAAGATTCCTGCGCACCCCAAGGTGAGATCGCCATCCTG 1080
QY 1081 GGTACCGCAAGGCGCGCTTACGAGAAGTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 1140
Db 1081 GGTACCGCAAGGCGCGCTTACGAGAAGTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCG 1140
QY 1141 CGCGCAAGGCGGTGCTCAAGTTCGCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCGCT 1200
Db 1141 CGCGCAAGGCGGTGCTCAAGTTCGCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCGCT 1200
QY 1201 GACTTCATGCTGCTGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCG 1260
Db 1201 GACTTCATGCTGCTGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCG 1260
QY 1261 CACTAGGTACCGTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCG 1320
Db 1261 CACTAGGTACCGTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCG 1320
QY 1321 GCGCTCACCGGTTCACATGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCT 1380
Db 1321 GCGCTCACCGGTTCACATGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCT 1380
QY 1381 GAGCGCGTGGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCT 1440
Db 1381 GAGCGCGTGGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCTTCGCGCGCT 1440
QY 1441 GAGATGTTGGCCAACTGATCAGCGAGGACTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db 1441 GAGATGTTGGCCAACTGATCAGCGAGGACTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1501 GAGGGCTGCTGAGGAGGTGGTGTACGCGCAAGGGCGGCTGCCACCGCCCAAGAGGAG 1560
Db 1501 GAGGGCTGCTGAGGAGGTGGTGTACGCGCAAGGGCGGCTGCCACCGCCCAAGAGGAG 1560
QY 1561 GAGATCAAGGTGCGCGCTTCGCGAGAGATCCCC 1593
Db 1561 GAGATCAAGGTGCGCGCTTCGCGAGAGATCCCC 1593
```

```

RESULT 2
AX049325 LOCUS
AX049325 DEFINITION
AX049325 Sequence 4 from Patent WO0071734.
AX049325 ACCESSION
AX049325.1 VERSION
GI:12226092
KEYWORDS
linear PAT 12-JAN-2001
```



```
|||||
Db 1561 GAGATCAAGGTGCCGTTGCGGAGATCCCC 1593
|||||
RESULT 3
AX049323
LOCUS AX049323
DEFINITION Sequence 2 from Patent WO0071734.
ACCESSION AX049323
VERSION AX049323.1 GI:12226090
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 2124).
AUTHORS D'Hulst,C. and Ball,S.
TITLE Starch granules containing a recombinant polypeptide of interest,
method for obtaining same and uses
JOURNAL Patent: WO 0071734-A 2 30-NOV-2000;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
Location/Qualifiers
1..2124
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="fragment de la sequence compl te de l'DNAc codant
la GBSSI de Chlamydomonas reinhardtii"
1..>2124
/notes="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC21780.1"
/db_xref="GI:12226091"
/transl_table="MAVASTSRPSPARPIVINAASFGVKKKTANOLLRELARGSARKST
SRGAVTCAATCALDIVMAAEVAPWMTGGLDVTGGLPIELVKKGRHVMITAPRY
DOYADADWTSVVDIMGEKRYFHSIKKGVHRVMDHPWFLAKVWGTGSKLYGPRSG
ADYLNDHRAINFCKAALAEARVLPFGPGEDCVFVANDWSALVPVLLKDEYQKQFQ
TKASVLAIINAIKPVGRWEEAFDKLPQAAEDKLPFSDGYAKVYIETATPEDEKRP
PLTGKTKKTNLWKGITIAADKLIVTSPTYATEIADAAGGVDELDTVIRAKGIEGIN
GMDIEENPTKFLSAPYQNSVYAGAAKEALQAEGLPVDPTAPLFAFIRLEE
OKGVDITLAALPKILAPKVOIALITGKAAEKLVAIGTKVGRKGVVFKFSAPLA
HMLTAGADEMLSPRPFCGLIOLHAMHYGTVPVASTGGLVDIVKGVTFHMGALN
PKLDEADALAAATVVRASEVAGGRYPENVANCISQDLSWSKPAKWGLLEEVY
KGGVATATKEELKPVPAEKIPGLDPAVSTAPNLKPVASVSENGAARAPKVGTIATA
MGWARTATPGSPFAAATPKVITLKPALPATAPKPTAGLKLAGEASTISUSENGAASN
GNGNGASAKTSKAPLVSAATRKSA"
BASE COUNT 369 a 773 c 656 g 326 t
ORIGIN
Query Match 100.0%; Score 1593; DB 6; Length 2124;
Best Local Similarity 100.0%; Pred. No. 2.2e-166;
Matches 1593; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGCTGGACATCGTGATGGTGTGCTGAGTTCGCCCTTGTGTCAAGACGGCGGCGCTG 60
Db 172 GCGTGGACATCGTGATGGTGTGCTGAGTTCGCCCTTGTGTCAAGACGGCGGCGCTG 231
Qy 61 GCGATGTGACTGTGGCTGCTTATGAGTGTGTCATGAGCGCGGCCACCGGCTCATGACC 120
Db 232 GCGGATGTGACTGTGGCTGCTTATGAGTGTGTCATGAGCGCGGCCACCGGCTCATGACC 291
Qy 121 ATTGCCCTCGCTAGCACGAGTACGCTACGCTGGGACACCTCGGTGGTGTGACATC 180
Db 292 ATTGCCCTCGCTAGCACGAGTACGCTACGCTGGGACACCTCGGTGGTGTGACATC 351
Qy 181 ATGGCGAGAGAGTCCGCTACTTCCATCCATCAAGAGGGCGTGACCGGCTGTGGATT 240
Db 352 ATGGCGAGAGAGTCCGCTACTTCCATCCATCAAGAGGGCGTGACCGGCTGTGGATT 411
Qy 241 GACCACCCCTGTTCTTGCCCAAGTCTGGGCGAAGACCGGCTCCAAAGCTGTACGGCCCC 300
Db 412 GACCACCCCTGTTCTTGCCCAAGTCTGGGCGAAGACCGGCTCCAAAGCTGTACGGCCCC 471
Qy 301 CGCTCGGGGCTGACTACTTGGACAAACCAAGCGCTTCGCCCTGTCTGCAAGSCCGCT 360
|||||
472 CGCTCCGCGCTGACTACTTGGACAAACCAAGCGCTTCGCCCTGTTCGAAGSCCGCT 531
361 ATTGAGGCTGCCGCGTGTCTCCCTTCGCGCCCGGCGAGGACTGCGTCTTCGTGGCCAAAC 420
532 ATTGAGGCTGCCGCGTGTCTCCCTTCGCGCCCGGCGAGGACTGCGTCTTCGTGGCCAAAC 591
421 GACTGGCAGCTCCGCGCTGTGGTCCCGTCTCTGCTGAAGGACGAGTACAGCCCAAGGGCCAG 480
592 GACTGGCAGCTCCGCGCTGTGGTCCCGTCTCTGCTGAAGGACGAGTACAGCCCAAGGGCCAG 651
481 TTCACCAAGGCGAAGTGGTGTCTGGCTATCCACACATATCGCTTCCAGGGCGGCGATGCG 540
652 TTCACCAAGGCGAAGTGGTGTCTGGCTATCCACACATATCGCTTCCAGGGCGGCGATGCG 711
541 GAGGAGGCTTTCAAGGACACGAGCTGCCCGCAGGCGCGCTTTTGACAAGCTGGCCTTCGCG 600
712 GAGGAGGCTTTCAAGGACACGAGCTGCCCGCAGGCGCGCTTTTGACAAGCTGGCCTTCGCG 771
601 GACGCTATGCGCAAGGTTTACACTGAGGCGCACCCCGCTGAGGAGGACGAGAGCCCGCG 660
772 GACGCTATGCGCAAGGTTTACACTGAGGCGCACCCCGCTGAGGAGGACGAGAGCCCGCG 831
661 CTGAGGGAAGACACTACAAGAGATCAACTGGCTGAAGGTGGCATTCATCGCCCGCGAC 720
832 CTGAGGGAAGACACTACAAGAGATCAACTGGCTGAAGGTGGCATTCATCGCCCGCGAC 891
721 AAGCTGTGACTGTGTCGCCCAACTACGCGACCGAGATCGCTTGCAGTGCGCCCGCGCGGT 780
892 AAGCTGTGACTGTGTCGCCCAACTACGCGACCGAGATCGCTTGCAGTGCGCCCGCGGT 951
781 GTGAGCTGGACACCGTTCATCGCGCCCAAGGCGCATTCAGGCGCATTCGACCGCGCATGGAC 840
952 GTGAGCTGGACACCGTTCATCGCGCCCAAGGCGCATTCAGGCGCATTCGACCGCGCATGGAC 1011
841 ATTGAGGAGTGAACCCCAAGACCGACAAAGTTCCTGTCTGCGCCCTACGACCAAGACAGC 900
1012 ATTGAGGAGTGAACCCCAAGACCGACAAAGTTCCTGTCTGCGCCCTACGACCAAGACAGC 1071
901 GTCTACGCGCGCAAGCGCGCCGCCCAAGGAGGCGCTTCGAGGCGGAGCTGGCGCTGCTGTG 960
1072 GTCTACGCGCGCAAGCGCGCGCCGCCCAAGGAGGCGCTTCGAGGCGGAGCTGGCGCTGCTGTG 1131
961 GACCCACCGCGCCCGCTGTTCGCTTCATCGCGCCCGCTGAGGAGGACGAGAGGCTGTGGAC 1020
1132 GACCCACCGCGCCCGCTGTTCGCTTCATCGCGCCCGCTGAGGAGGACGAGAGGCTGTGGAC 1191
1021 ATCATCTCTGGCGCGCTTCGCCCAAGATTCCTGGCCACCCCAAGGTGCAGATCGCCATCTCTG 1080
1192 ATCATCTCTGGCGCGCTTCGCCCAAGATTCCTGGCCACCCCAAGGTGCAGATCGCCATCTCTG 1251
1081 GGTACCGCGCAAGCGCGCGCTTCGAGAGGCTGTGTAAGCGCATCGGCACCAAGTACAGGCGC 1140
1252 GGTACCGCGCAAGCGCGCGCTTCGAGAGGCTGTGTAAGCGCATCGGCACCAAGTACAGGCGC 1311
1141 GCGCGCAAGGCGGCTGGTCAAGTTCCTGGCGCCCGCTGGCGCACATCTCACCGCGCGCGCC 1200
1312 CCGCGCAAGGCGGCTGGTCAAGTTCCTGGCGCCCGCTGGCGCACATCTCACCGCGCGCGCC 1371
1201 GACTTCATCTGCTGGTGGCTTCGAGCGCTTCGAGCGCTTCGCGCGCTATCCAGCTGCACGCGATG 1260
1372 GACTTCATCTGCTGGTGGCTTCGAGCGCTTCGAGCGCTTCGCGCGCTATCCAGCTGCACGCGATG 1431
1261 CACTACGCTTACCGTGGCTGGTAGCCTCCACCGCGCGCGCTGGTGACACCGCTCAAGGAG 1320
1432 CACTACGCTTACCGTGGCTGGTAGCCTCCACCGCGCGCGCTGGTGACACCGCTCAAGGAG 1491
1321 GCGCTACCGGCTTCCACATGGGCGCGCTGAAACCCCGCAAGCTGACGAGCTGACGCGC 1380
1492 GCGCTACCGGCTTCCACATGGGCGCGCTGAAACCCCGCAAGCTGACGAGCTGACGCGC 1551
1381 GACGCGCTGGCGCGCACCGTGGCGCGCTGCGACGAGCTGTTGCGGCGCGCGCTACCGCC 1440
|||||
```



```
QY 721 AAGCTGGTGAAGTGTGCGCCCACTACGACGACGAGATCGCTGCCGATGCCGCGGGGT 780
|||||
Db 721 AAGCTGGTGAAGTGTGCGCCCACTACGACGACGAGATCGCTGCCGATGCCGCGGGGT 780
QY 781 GTGAGTGTGACACGCTATCCGCGCAAGGCGATTTGAGGCGATTTGTAACGGCATGGAC 840
|||||
Db 781 GTGAGTGTGACACGCTATCCGCGCAAGGCGATTTGAGGCGATTTGTAACGGCATGGAC 840
QY 841 ATTGAGAGTGGACCCCAACGACGACAGTTCCTGTCTGGCCCTAGCAGCAGACAGC 900
|||||
Db 841 ATTGAGAGTGGACCCCAACGACGACAGTTCCTGTCTGGCCCTAGCAGCAGACAGC 900
QY 901 GTCTACGCGCGCAAGGCGCGCCCAAGGAGGCGCTGCAAGCGCGAGCTGGGCTGGCTGTG 960
|||||
Db 901 GTCTACGCGCGCAAGGCGCGCCCAAGGAGGCGCTGCAAGCGCGAGCTGGGCTGGCTGTG 960
QY 961 GACCCCAAGCGCGCGCTGTCCTTCATCGCGCGCTGGAGGAGCAGAGGGTGTGGAC 1020
|||||
Db 961 GACCCCAAGCGCGCGCTGTCCTTCATCGCGCGCTGGAGGAGCAGAGGGTGTGGAC 1020
QY 1021 ATCATCTGGCGCGCTGCCCAAGATCTGCGCCACCCCAAGGTGACATGCCATCCTG 1080
|||||
Db 1021 ATCATCTGGCGCGCTGCCCAAGATCTGCGCCACCCCAAGGTGACATGCCATCCTG 1080
QY 1081 GGTACGCGCAAGGCGCGCTACGAGAGTGTGACGCGCATCGGCACCAAGTACAGGCG 1140
|||||
Db 1081 GGTACGCGCAAGGCGCGCTACGAGAGTGTGACGCGCATCGGCACCAAGTACAGGCG 1140
QY 1141 CGCGCAAGGCGGTGCAAGTTCGCGCGCGCTGGCGGCACATGCTACCGCGCGCGCC 1200
|||||
Db 1141 CGCGCAAGGCGGTGCAAGTTCGCGCGCGCTGGCGGCACATGCTACCGCGCGCGCC 1200
QY 1201 GACTTCATGCTGGTCCCTCGCGCTTCGAGCGCTCGCGCGCTGATCCAGCTGACCGCCATG 1260
|||||
Db 1201 GACTTCATGCTGGTCCCTCGCGCTTCGAGCGCTTCGAGCGCTGATCCAGCTGACCGCCATG 1260
QY 1261 CACTACGCTACGTCGCGCTGGTGTGAGCTTCACCGCGCGCGCTGGTGTGACACCGCTC 1314
|||||
Db 1261 CACTACGCTACGTCGCGCTGGTGTGAGCTTCACCGCGCGCGCTGGTGTGACACCGCTC 1314

RESULT 7
AF433156 5856 bp DNA linear PLN 23-AUG-2002
LOCUS Chlamydomonas reinhardtii granule-bound starch synthase I (STA2)
DEFINITION gene, complete cds.
ACCESSION AF433156
VERSION AF433156.1 GI:16755882
KEYWORDS Chlamydomonas reinhardtii.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
REFERENCE 1 (bases 1 to 5856)
AUTHORS Watebled,F., Buleon,A., Bouchet,B., Ral,J.P., Lienard,L.,
Dauvillee,D., Bunderup,K., Dauvillee,D., Ball,S. and D'Hulst,C.
TITLE granule-bound starch synthase I: a major enzyme involved in the
biogenesis of B-crystallites in starch granules
JOURNAL Eur. J. Biochem. 269 (15), 3810-3820 (2002)
PUBMED 12153578
REFERENCE 2 (bases 1 to 5856)
AUTHORS Watebled,F., Ball,S.G. and D'Hulst,C.
TITLE Direct Submission
JOURNAL Submitted (15-OCT-2001) UMR8576 du CNRS, Laboratoire de Chimie
Biologique, Université des Sciences et Technologies de Lille,
Villeneuve d'Ascq CEDEX 59655, France
FEATURES
source
location/Qualifiers
1..5856
/organism="Chlamydomonas reinhardtii"
/db_xref="taxon:3055"
1343..>4911
/gene="STA2"
join(1343..1781,2151..2340,2484..2618,2815..2973,
```

```
3186..3373,3582..4117,4295..4911)
/gene="STA2"
/product="granule-bound starch synthase I"
join(1480..1781,2151..2340,2484..2618,2815..2973,
3186..3373,3582..4117,4295..4911)
/gene="STA2"
/note="similar to the sequence deposited in GenBank
Accession Number AF026420; GBSSI"
/codon_start=1
/product="granule-bound starch synthase I"
/protein_id="AAL28128.1"
/db_xref="GI:16755883"
/translation="MAVASTRSPSSARPIVINAASFVKKTAANOLLRELARGSARKST
SRSAVTGATGATCADIIVMAAEVAPWSKTGGDVTGGLEIELVKGRHVMITAPRY
DYADAWDTISVVDMIGEHKVFHSHIKKGVHRVWDHPFLAKVMGKTGSKLYPRSG
ATYLDNHRKFAFCFCAALEAAEAVLPFGEDCVFANDHSAVLPVLLKDEYQPKGQF
KSKYLAIHNIAPFGWEEAFKDKLPQAAFDKLPFADSGYAKVYTEATMEDEKP
PLTKSTYKKNWLGIIIAADKLVTSNRYATEIAADAAGGVELDVTIRAKISGIVN
GMDIEWNPKTDKFLSVYDQNSVTAGKAAKEALQALGLPVDPTAPLPAFIRLEE
QKGVDIITLALPKILATPKVQIILGTGKAAEKLVAIGIKYKGRAGVVKFSAPLA
HMLTAGADEMLVPSRFEPGLIQLHAMHYGTVPVASTGGGLVDVTKGVTGFHMGALN
PKLTADEADADALATVRRASEVFGAGRYPENVANCISQDLSPKPAQKEGLLEEVY
GKGVATAKKEEIKVPVAKETPGDLPVSYAPNTLKPVSVEGNGAAAPKVGITAPA
MGNRATTPSPSPAATPKVTVKYPALPAKPKTAGLKLAGEASTTSTSENGAASN
GNGNGASAKTSAAKPLVSAATKSA"
BASE COUNT 1073 a 1816 c 1852 g 1115 t
ORIGIN
Query Match 37.9%; Score 603.8; DB 8; Length 5856;
Best Local Similarity 81.2%; Pred No. 6.6e-58;
Matches 795; Conservative 0; Mismatches 7; Indels 177; Gaps 1;
QY 792 CACCGTCATCCGCGCAAGGCGCATTTGAGGCGCATTTGTGAACGGCGATGGACATTTGAGGAGTG 851
|||||
Db 3570 CTCCTCCCGCAGCGCCAGGCGCATTTGAGGCGCATTTGTGAACGGCGATGGACATTTGAGGAGTG 3629
QY 852 GAACCCCAAGACCGACAAAGTTCTCTGTCTGCGCCCTACGACCGACGACGCTCTACCCCGG 911
|||||
Db 3630 GAACCCCAAGACCGACAAAGTTCTCTGTCTGCGCCCTACGACCGACGACGCTCTACCCCGG 3689
QY 912 CAAGCGCGCGCGCAAGGAGCGCTCGAGCGCGAGCTGGCGCTGGCGCTGTGAGACCCCGC 971
|||||
Db 3690 CAAGCGCGCGCGCAAGGAGCGCTCGAGCGCGAGCTGGCGCTGGCGCTGTGAGACCCCGC 3749
QY 972 CCCCCTGTTGCGCTTCATCGCGCGCTGGAGGAGCAGAGGGTGTGGACATCATCTCTGCG 1031
|||||
Db 3750 CCCCCTGTTGCGCTTCATCGCGCGCTGGAGGAGCAGAGGGTGTGGACATCATCTCTGCG 3809
QY 1032 CGCCCTGCGCAAGATCTCTGCGCACCCCGCAAGGTGCGAGATCGCCATCTCTGGTACCGGCAA 1091
|||||
Db 3810 CGCCCTGCGCAAGATCTCTGCGCACCCCGCAAGGTGCGAGATCGCCATCTCTGGTACCGGCAA 3869
QY 1092 GGCGCGCTACGAGAAGCTGTGAACGCCATCGGCACCAAGTACAAAGGCGCGCGCCCAAGG 1151
|||||
Db 3870 GGCGCGCTACGAGAAGCTGTGAACGCCATCGGCACCAAGTACAAAGGCGCGCGCCCAAGG 3929
QY 1152 CFTGTFCAAGTTCTCGCGCGCGCTGGCGCACATGCTCACCGCGCGCGCGGACTTCACTGCT 1211
|||||
Db 3930 CFTGTFCAAGTTCTCGCGCGCGCTGGCGCACATGCTCACCGCGCGCGCGGACTTCACTGCT 3989
QY 1212 GGTGCGCTCGCGCTTCGAGCGCTCGCGCTGATCCAGCTGACGCCATCGCTGACCTACGGTAC 1271
|||||
Db 3990 GGTGCGCTCGCGCTTCGAGCGCTCGCGCTGATCCAGCTGACGCCATCGCTGACCTACGGTAC 4049
QY 1272 CFTGCGCGGTGTAGCTCCACCGCGCGCTTGTGTCGACACCGTCAAGGAGGCGGTTCACCGG 1331
|||||
Db 4050 CFTGCGCGGTGTAGCTCCACCGCGCGCTTGTGTCGACACCGTCAAGGAGGCGGTTCACCGG 4109
QY 1332 CTTCCACA----- 1339
|||||
Db 4110 CTTCCACAGTACGCGGGGCTTCGCTGGTGGTGTGAATTTGTCCCTGAAGTGGTTCGTT 4169
QY 1340 ----- 1339
```


Db 4170 GCGGGGCGCTTGACGGGCTCTCTGACAGTCTCTACCTCTGCTGCGCGCGCCAGGAACCC 4229
 QY 1340 ----- 1339
 Db 4230 ACCGATATCGGAGACACCGTGGCGCATGCTGACGGCTCCCTTTTCCCTCTGTTCCCTGAT 4289
 QY 1340 -----TGGCGCGCTGAACCCGACAAAGCTGGACGAGGCTGACCGCAGCGCTGCGCGC 1394
 Db 4290 CCGAGTGGCGCGCTGAACCCGACAAAGCTGGACGAGGCTGACCGCAGCGCTGCGCGC 4349
 QY 1395 CACCGTGGCGCGCTGACGAGGCTGTTTGGCGCGCGCTGACCGCAGATGGTGGCCAA 1454
 Db 4350 CACCGTGGCGCGCTGACGAGGCTGTTTGGCGCGCGCTGACCGCAGATGGTGGCCAA 4409
 QY 1455 CCGCATCAGCAGGAGGCTGCTGCTGCTCAAGCCGCGCGCGCGCGCGCGCTGCTGGA 1514
 Db 4410 CTGCATCAGCAGGAGGCTGCTGCTGCTCAAGCCGCGCGCGCGCGCGCTGCTGGA 4469
 QY 1515 GGAGTGGTGTACGGCAAGCGCGCTGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCG 1574
 Db 4470 GGAGTGGTGTACGGCAAGCGCGCTGCGCCACCGCGCGCGCGCGCGCGCGCGCGCG 4529
 QY 1575 CGTTCGCGAGAGATCCCC 1593
 Db 4530 CGTTCGCGAGAGATCCCC 4548

RESULT 8
 AF286320
 LOCUS
 DEFINITION
 Triticum aestivum granule bound starch synthase I (GbsSI) gene,
 complete cds.
 ACCESSION
 AF286320
 VERSION
 AF286320.1 GI:11037535
 KEYWORDS
 Triticum aestivum.
 ORGANISM
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 2289)
 McCue,K.F., Hurkman,W.J., Tanaka,C.K. and Anderson,O.D.
 Starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum
 aestivum cv. Cheyenne): Molecular Characterization, Developmental
 Expression, and Homolog Assignment by Differential PCR
 Unpublished
 2 (bases 1 to 2289)
 McCue,K.F. and Anderson,O.D.
 Direct Submission
 Submitted (11-JUL-2000) United States Department of Agriculture,
 Agricultural Research Service, 800 Buchanan Street, Albany, CA
 94710-1105, USA

FEATURES
 source
 1. 2289
 /organism="Triticum aestivum"
 /cultivar="Cheyenne"
 /db_xref="taxon:4565"
 /tissue_type="endosperm"
 204..2021
 /gene="GbsSI"
 204..2021
 /gene="GbsSI"
 /EC_number="2.4.1.21"
 /note="glucosyltransferase; ADP glucose glucosyl
 transferase; waxy; Wx"
 /codon_start=1
 /product="granule bound starch synthase I"
 /protein_id="AAC27624.1"
 /db_xref="GI:11037536"
 /translation="MAALVTSQATSLGILTRFRAGFGQVRPRSPADAPLGMRT
 TGAAPKQSRKRAHGRTRCLSMVYRATSGAGNLVFGAEMAPSKTGLGLVGG
 LPPMAANGHRVMVISPVDQYKDAWDISVSEIKVADEYERYFHCYKRGVDRVFV

DHPCFLEKVRGKTKKIYGPDACTDYEDNOLRSLICQAALAPRILDLNNNPFSSP
 YGEDVYFVNCNDWHTGLLACYLKSNYOSSGIYRTAKVAFCHLNISYOGRSFDDPAQLN
 LDRFKSSPFDIDGYDKPVGBKINMKAGIILQADKVLVSPYPAELLSEARGCEL
 DNIMRLTGITGIVNGMDVSEWDPAKFLAANDVDTTALLEGKALNEALQAEVGLPVD
 RAVPLVAFIGRLUEQKQPDVMTAAIPEILKEEDVQIVLLTGKKFERLLKSVEEKFP
 SKVRVRFENAPLAHOMAGADVLAIVSRFEPCLQLQGMRYGTPTCACTAGTGLVDT
 IMEGKTGFHMHLSVDCNVVEPADVKVVTTLKRAVKVGTTPAYHEMWKNCMIQDLISW
 KGPAPKNWEDVLLLEIGVEGSEPGVIGIEIAPLAWENVAAP"

BASE COUNT 480 a 684 c 735 g 390 t
 ORIGIN

Query Match 33.6%; Score 535.8; DB 8; Length 2289;
 Best Local Similarity 61.8%; Pred. No. 2.5e-50;
 Matches 1008; Conservative 0; Mismatches 527; Indels 96; Gaps 6;

QY 5 TGGACATCGTGTGTTGCTGAGTCCGCCCTTGGTCCAAGAGCGGGCGGCTGGCG 64
 Db 436 TGNACCTCGTGTGCTGCGCGCGAGATGGCCCTTGGAGCAAGACGGCGGCTCGCG 495
 QY 65 ATGTGACTGGTGGCCCTGCTTATTGAGTGGTCAAGCGCGGCCCGCTCATGACCATG 124
 Db 496 AGTCTCTCGGGGCTCCGCCAGCCATGSCCGCAACGGTCAACCGGCTCATGTCATCT 555
 QY 125 CCCCTCGCTACGACAGTACGCTGACCGCTGGGACACCTGGTGGTGGACATCATGG 184
 Db 556 CCCCAGCTACGACAGTACGAGGAGCGCTGGGACACCGAGCGCTCTCGAGATCAAGG 615
 QY 185 -----GCGAGAAGGTCCGCTACTTCCACTCCATCAAGAGGGGCTGCACCGCG 232
 Db 616 TCGCGGACGAGTACGAGAGGGTGGAGTACTTCCACTGCTACAGCGCGGGGTGGACCGG 675
 QY 233 TGTGGAITGACCAACCCCTGTTCTTGGCCAAAGTCTGGGGCAAGACCGGCTCCAAAGTCT 292
 Db 676 TGTTCGTGACCAACCCGCTGCTTCTTGGAGAGGTCCGGGCAAGACCAAGGAGAAATCT 735
 QY 293 AGGCGCCCGCTCGCGCGCTGACTGACCTGGACCAACCAAGCGCTTGGCCCTGTTCTGCA 352
 Db 736 AGGCGCCGATCGCGGACGAGTACGAGGAGCAACAGCTACGCTTCAGCCTGCTCTGCC 795
 QY 353 AGGCGCTATTGAGGTGCGCGGCTGCTGCCCTTC-----G 388
 Db 796 AGGCGCGCTTGGGACCGCCAGGATCCTCGACTCAACCAACCCCATACTTCTCGGAC 855
 QY 389 GCCCGCGGAGGACTGCTTCTTGGCCAAAGTCTGGGCAAGTCCGCCCTGGTGGCGCTCC 448
 Db 856 CCTACGGGGAAGACGTGTTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 915
 QY 449 TGTGAAGACGAGTACGACGCGGCGGCTTCCAGGCGGCGGCTTCCAGGCGGCGGCTGTA 508
 Db 916 ACCTCAAGAGCAACTACCACTGCTGAGTCCAGTCCAGGCGGCGGCTTCCAGGCGGCGG 975
 QY 509 TCCCAACATCGCTTCCAGGCGGCGGCTTCCAGGCGGCGGCTTCCAGGCGGCGGCTTCCAG 568
 Db 976 TCCCAACATCTGATCAGGCGGCGGCTTCTCTTCCAGGCGGCTTCCAGGCGGCGGCTTCCAG 1035
 QY 569 CCGAGCGCGCTTTCAGCAAGCTGCGCTTTCGAGCGGCTTTCGAGCGGCTTTCAGCTGAGG 628
 Db 1036 CCGACAGGTTCAGGTCGCTTTCGACTTTCGAGCGGCTTTCAGCTGAGGCTTTCAGCTGAGG 1082
 QY 629 CCACCCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 688
 Db 1083 -----CCGGTGGAGGCGCG-----AAGATCA 1104
 QY 689 ACTGCTGAAGGTGGCATTAATGCGCGCGGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 748
 Db 1105 ACTGATGAAGCGCGGAGTCTGCGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1164
 QY 749 CGACCGGAGTGGTGGCGGATGCGCGCGGCGGCTGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 808
 Db 1165 CGGAGGAGTCTCTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1224
 QY 809 AGGCATGAGGCGATTGTGAACCGCATGAGGAGTGGAGGAGTGGAGGAGTGGAGGAGTGGAGGAG 868

Db 1225 CGGACATACCGGCTCGTCAACGGCATGACGTCAGAGAGTGGACCCCGCCAAAGGACA 1284

QY 869 AGTTCCTGTCTGCGCCCTAGACACAGACGCTCTACGCGGCAAGCGCGCCGCCAAGG 928

Db 1285 AGTTCCTGCGCGCACTACGACGTCACCGGCTTGGAGGAGAGCGCTGAAACAGG 1344

QY 929 AGGCGCTGCAAGCGGAGCTGGGCTGCTGTGACCCGACCGCCCGCTGTTCGCTTCA 988

Db 1345 AGGCGCTGCAAGCGGAGCTGGGCTGCGGTGGACCGGAGGTCGCTGTGCGCTTCA 1404

QY 989 TCGCGCGCTGGAGAGCAGAGAGGTGTGACATCATCTTGGCGCGCGCTGCCAAGATCC 1048

Db 1405 TCGCGAGCTGGAGAGCAGAGAGGCGCGCGCTGATGATGCGCGCATCCCGGAGATCT 1464

QY 1049 TGGCCACCCCAAGTGCAGATGCCATCTGCTGGTACCGGCAAGCGCGCTTACGAGAAGC 1108

Db 1465 TGAAGGAGGAGGAGCTCGATGCTCTCTGGGACCGGGAAGAGAGTTCGAGCGG 1524

QY 1109 TGTGAACCGCATCGGACCAAGTACAGAGCGCGCGCAAGGGGTGTGTCAGTCTTCGG 1168

Db 1525 TGCTCAAGAGCGTGGAGAGAGTTCGCGAGCAAGGTGAGGCGGTGTGTCAGGTTCAACG 1584

QY 1169 CGCCCTGGCGGCATGCTACCGCGCGCGCGGACTTCATCTGCTGTCGCTGCGGCTTCG 1228

Db 1585 CGCGCTGGCTACACAGATGATGCGCGCGCGGACGCTGCTCGCGCTACACGCGGCTTCG 1644

QY 1229 AGCCCTGGCGGCTGATCCAGCTGCACGCCATCGACTACGCTACCGTGCCTGCTGAGCT 1288

Db 1645 AGCCCTGGCGGCTGATCCAGCTGCAGGGATGCGCTACGGAACCGCGTGCCTGCGGT 1704

QY 1289 CCACCGCGGCGCTGCTGACACCGCTCAAGAGGCGGTCAACCGGTTCACATGCGCGGCC 1348

Db 1705 CCACCGCGGCGTCTGTCACACGATCATGAGGCGCAAGACCGGTTCCACATGCGCGCAC 1764

QY 1349 TGA-----ACCCGCAAGCTGGACAGGCTGAGCGCGGCGGCGCGCTGCGCGCTGCG 1402

Db 1765 TCAGCGTGCATGCAACGTGTGTGAGCGCGCGGCTGAAGAGGTGTGAGCCACCTGA 1824

QY 1403 GCGTGCAGCGAGGTGTTTGGCGCGCGCTACCCGAGATGTGTGCGCAACTGCATCA 1462

Db 1825 AGCGCGCGTCAAGTCTGCGCAGCGCGAGCTACCATGATGTCAAGAACTGCATGA 1884

QY 1463 GCGAGGACTGCTGCTGCTCAAGCGCGCGCAAGAGTGGAGGCGCTGCTGGAGGAGTGG 1522

Db 1885 TCCAGGATCTCTCTGGAAGGCGCGCAGCAAGAACTGGAGGACGTGCTTCTGGAACGTG 1944

QY 1523 TGTACGCAAGCGCGGCTGGCCACCGCCCAAGAGGAGGATCAAGTGTGCGCTTGGCG 1582

Db 1945 GG---GTGAGGGGAGCGAGCCAGGGTTCATCGCGGAGGAGATTCGCGGCTCGCCATGG 2001

QY 1583 AGAAGATCCC 1593

Db 2002 AGAAGTGC 2012

RESULT 9
AF486514
LOCUS
DEFINITION AF486514 1812 bp mRNA linear PLN 02-JUL-2002
Hordeum vulgare cultivar oderbrucker granule bound starch synthase
I mRNA, complete cds.

ACCESSION AF486514
VERSION AF486514.1 GI:21667427
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 1812)
Patron, N., Smith, A., Fahy, B., Hylton, C., Naldrett, M., Rossnagel, B.
and Denyer, K.
A mutation in the 5' non-coding region of the barley GBSSI gene
alters its temporal and spatial expression and reduces GBSSI

activity and amylose content in the endosperm
Unpublished
2 (bases 1 to 1812)
Patron, N.
Direct Submission
Submitted (22-FEB-2002) Metabolic Biology, John Innes Centre,
Norwich Science Park, Norwich, Norfolk NR4 7UH, UK
JOURNAL
TITLE
JOURNAL
FEATURES
Location/Qualifiers
1. 1812
/organism="Hordeum vulgare"
/cultivar="oderbrucker"
/db_xref="taxon:4513"
1. 1812
/note="alpha glucosyl transferase"
/codon_start=1
/product="granule bound starch synthase I"
/protein_id="AAW74048.1"
/db_xref="GI:21667428"
/translation="MAALATLSQATSGTVLGVDFRRPFGQGLRPNPADALGMRT
IGASAPKQSKAHRSRSLSVVVSATGSMNLFVGAEMAPWSKGGGLDVLGLP
PAMAANGHRVWSPRYDQYKADWDIYSIEKVADYERFHFYKRVDRVFIH
PWLEKVRGKTKEIYGDAGTDYDQRFSLQALAEPRILNINNNYFSGPLP
EDVVEVCNDWHTGLLACYLSNYGKINMGKILQADKVLTVSPYAEELISGEARGELDN
DRKSSDFIDGDKPVGGRKINMGKILQADKVLTVSPYAEELISGEARGELDN
IMRLTGIIVNGMDVSEWDPDKFLAVNYDJTALAEKALKEALQAEVGLPDKR
VPLVAFIGRLEEQKQPDVPIAIPILKEEDVQIILGTGKKKEKLLKSMEEKPPGK
VRVAFRENAFLAHQMAGADILLAVTSRPECGLILOLMGMYGTGTCVCASTGIVDIIY
EGKTGFHMGRLSDVNCVNPVADKKVATLTKRAVYVGTGTPAYOEMVKNCMIDLSWKG
PAKNWEDVLELGVGSGRPVIGVEIAPLAMEVAAAP"
BASE COUNT 363 a 564 c 597 g 288 t
ORIGIN
Query Match 33.3%; Score 530; DB 8; Length 1812;
Best Local Similarity 61.6%; Pred. No. 1.2e-49;
Matches 985; Conservative 0; Mismatches 520; Indels 93; Gaps 5;
QY 5 TGCACATCGTGTGCTGCTGAGTGCCTTGTGTCCTCAAGAGCGGCGCTGGGCG 64
Db 227 TGAACCTCGTGTTCGCGCGCGAGATGCGCGCTTGGAGCAAGACCGCGCTGGCG 286
QY 65 ATGTGACTGTGGCTGCTGCTATTGAGCTGTGTCGAGCGCGCCACCGCTGATGACCATG 124
Db 287 ATGTCTCGCGGCGCTCCCGCGGCGCATGCGCGCAACGGTCAACGGGTGATGCTGTCT 346
QY 125 CCGCTGCTACGACAGTACGCTGACGCTGGACCTGGAGCTGCTGGTGGTGGACATCATG 184
Db 347 CCGCGCGCTACGATCATGATCAAGAGCGCTGGGACACCAAGCGTCATCTCCGAGATCAAG 406
QY 185 -----GCGAGAAGTCCGCTACTTCCACTCCATCAAGAGGCGCTGACCGCG 232
Db 407 TCGCTACAGAGTACGAGAGGTGAGGTTCCTCCACTGCTACAAGCGGAGTGGACCGCG 466
QY 233 TGTGATTGACCAACCGCTGCTTCTTCTGCGCAAGTCTGCGGCAAGACCGGCTCCAACTGT 292
Db 467 TGTTCATGACCAACCGCTGCTTCTTCTGCGCAAGTCTGCGGCAAGACCAAGAGATCT 526
QY 293 AGGCGCGCGCTCCCGCGCTGCTTCTTCTGCGCAAGTCTGCGGCAAGACCGGCTCCAACTGT 352
Db 527 AGGCGCGCGCGCTCCCGCGCTGCTTCTTCTGCGCAAGTCTGCGGCAAGACCAAGAGT 586
QY 353 AGGCGCGCTATTGAGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 388
Db 587 AGGCGCGCTATTGAGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
QY 389 GCGCGCGCGAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 448
Db 647 CTTACGGGGAAGACGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
QY 449 TGTGAGGAGGAGTACCGAGCG 508
Db 707 ACCTCAAGAGCAACTACCACTGCTCAATGGCATCTACAGGAGCGCGCGCGCGCGCGCGCG 766
QY 509 TCCACAACATCGCTTCCAGGCG 568

```
|||||
767 TCACAAACATCTCGTACAGGCGCGTCTCTCTTCCAGACATTGCGCAGCTCAACCTGC 826
QY CCCAGGCGCCCTTTGACAAAGCTGGCTCTTCGAGCGGCTAIGCAAAGTTTACACTGAGG 628
Db CGACAGGTTCAAGTCTGCTCTTCTGACTTATTCAGCGCTACGACAAG----- 873
QY CCACCCCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 688
Db -----CCCTGGAGGGGGG-----AAGATCA 895
QY ACTGGCTGAAGGCTGCAATATGCGCGGACAAAGCTGGTGAAGTGTGCTGCCCAACTACG 748
Db ACTGGATGAAGGCGGGATCTTCAGGCGGACAAAGTGTGAGGTTGAGCCCTACTACG 955
QY CGACCCAGATCGCTGCGGATGCGCGGCGGCTGAGAGTGGACACCGTATCCCGGCCA 808
Db CTGAGGAGCTCATCTCTGCGGAGGCGGAGGCTGCGAGCTCGACACATCATCGCCTCA 1015
QY AGGGCAITCAGGCGATTGTGAAGCGCATGACATTCAGAGTGGACACCGTATCCCGGCCA 868
Db CGGGATACCGGATCTCAAGCGCATGAGCGTCAAGTGGAGGAGGAGGAGGAGGAGGAG 1075
QY AGTCTCTGCTCGGCTTACGACCAAGAGCGGTCTTACCGCGGCAAGCGCGCGCAAGG 928
Db AGTCTCTCGGCTCAACTACGACATCAACACCGGCTTGAGGCCAAGGCGCTGAACAAG 1135
QY AGGCGCTTCAGCGCCAGCTGGCGCTGCTGTGACCCCAAGCGCGCGCTGTGCGCTTCA 988
Db AGGCGCTTCAGCGCCAGCTGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTTCA 1195
QY TCGGCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1048
Db TCGGCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1255
QY TGGCCACCCCAAGTGCAGATTCGCTTGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 1108
Db TGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1315
QY TGGTCAAGCCCATCGGACCAAGTACAGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 1168
Db TGCTCAAGAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1375
QY CGCCCTCGGCGCATGCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1228
Db CGCGCTAGCTCACAGATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1435
QY AGCCCTCGGCGCATGCTCACAGTGCACGCGATGCTACGCTACGCTACGCTACGCTACGCT 1288
Db AGCCCTCGGCGCATGCTCACAGTGCACGCGATGCTACGCTACGCTACGCTACGCTACGCT 1495
QY CCACCGCGCGCGCTGCTGACACCGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1348
Db CCACCGCGCGCGCTGCTGACACCGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1555
QY TGA-----ACCCGACAAAGTGGACGAGGCTGACGCGGAGGAGGAGGAGGAGGAGGAGGAG 1402
Db TCAGCGTTCGACTGCAACGCTGTGGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1615
QY GCGGTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1462
Db AGCGGGCGCGTCAAGTCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1675
QY GCCAGGAGCTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1522
Db TCCAGGATCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1735
QY TGTACGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Db GGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1773
```

RESULT 10

```
HWAXYR
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source
CDS
polyA_site
polyA_site
polyA_site
BASE COUNT
ORIGIN
Query Match
Best Local Similarity
Matches
QY 5 TGGACATCGTGATGGTTCGTCTGCTGAGGTCGCGCCCTTGGTCCAAAGACGCGCGCGCTGGCGG 64
Db 452 TGAACCTCGTGTCTGTCGCGCGCGAGATGGCGCCCTGGAGCAAGACCGCGCGCTGGCGG 511
QY 65 ATGTGACTGTGGCGCTGCTTATGTAGCTGGTCAAGCGGCGGCGGCGGCGGCGGCGGCGG 124
Db 512 ATGTCTCGGCGCGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 571
QY 125 CCCCTCGCTACGACGAGTACGCTGAGCGCTGGGACACCTCGGCTGCTGCTGACATCATGG 184
Db 572 CCCCGCTACGATCAGTACAGGAGCGCTGGGACACCGGCGGCGGCGGCGGCGGCGGCGG 631
HWAXYR
2311 bp mRNA linear PLN 12-SEP-1993
Barley mRNA pcwx27 for waxy locus.
X07932
X07932.1 GI:19128
starch synthase; waxy locus.
Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 2311)
Zohde, W.
Direct Submission
Submitted (21-JUN-1988) Zohde W., Max Planck Institute, Erwin Baur
Institut, D-5000 Koln 30, FRG
2 (bases 1 to 2311)
Rohde, W., Becker, D. and Salamini, F.
Structural analysis of the waxy locus from Hordeum vulgare
Nucleic Acids Res. 16 (14B), 7185-7186 (1988)
88303345
2970062
The sequence overlaps with the genomic sequence of the waxy locus,
x07931, from bp 1918 to bp 2301.
Location/Qualifiers
1..2311
/organism="Hordeum vulgare subsp. vulgare"
/strain="Vogelsanger Gold"
/db_xref="taxon:112509"
/map="chromosome 1"
/clone="pcwx27"
/clone_lib="EMBL4"
226..2037
/note="starch synthase"
/codon_start=1
/protein_id="CAA30756.1"
/db_xref="GI:19128"
/db_xref="SWISS-PROT:P09842"
/translation="MAALATSLATSGTGLVGTDRFRPFGQLRPNPADAALGMRT
IGASAAKQSRKAHRGSRCLSVVSATSGSMNLVFGAEAPWSTGGLGVLGGLP
PAMRANGHRVWVSPRYQYKADWTSIVSEIKVADEYERVFHYKRGVDRFIDH
PWFLEKVRGKTEKTYGPDAGTDEDNQORFSLCQAALAPRLINNNYFSGPYG
EDVVEVCNDWHITGLLACYLKNYSNGYRTAKVAFCHINISYGRFDFDPAQNLNLP
DRFKSDFIDGYDKPVEGRKINWKGALQADKLVTSYVYAEELISGEARGCLDN
IMRLTGITGVNGMDVSEWDTKDFLAVNYDITTALEKALKALKEALGVLPLVDRK
VPLVAFIGRLPEQGPDMVIAAIPILKEEDVQIILCTGKKKFKLLKSMEEKPPGK
VRVVRNAPLAHOMAGADLLAVTSREPEGLIQLQMRVGTGTCVCASTGGGLVDITV
EGKTFHNGRLSVDCNVVPEADVKVATILKRAVKVGTGPAYQEMVKMCMQDLSWKG
PAKRWEDVLLLELGVGSEPGIVGEEIAPLAMENVAAP"
2276
/note="poly A site (pcwx4)"
2283
/note="poly A site (pcwx27)"
2301
/note="poly A site (pcwx18)"
501 a 688 c 714 g 408 t
Score 530; DB 8; Length 2311;
Pred. No. 1.1e-49;
Conservative 0; Mismatches 520; Indels 93; Gaps 5;
```

QY 185 -----GGAGAAGTCCGCTACTTCCACTCCATCAAGAAGGGCGGTGACCGCG 232
Db 632 TCGCTGACGAGTACGAGAGGTGAGGTCTTCCACTGCTCAAGCGGGAGTGGACCGG 691
QY 233 TGTGATTGACACCCCTGTTCTGCGCAAGTCTGSGGCAAGACCGGCTCCAAAGTGT 292
Db 692 TGTTCATGACACCCGCTGTTCTGAGAAAGTCCGGGGCAAGACCAAGGAGAAGTCT 751
QY 293 ACGGCCCCGCTCGGCGCTGACTACCTGGACCAACCAAGCGCTTCGCCCTGTCTGCA 352
Db 752 ACGGCCCCGACGCGCGCACACTATGAGGACCAACCAAGCGCTTCAGCCTTCTGCCC 811
QY 353 AGGCGCTATTGAGGCTCCCGCGCTGCGCTTC-----GG 388
Db 812 AGGAGACTCGAGGACCCAGGATCTCACTCAACAACACCCCTACTTTCGTGTC 871
QY 389 GCCCGGGGAGAGTCTGCTGTCGCGCAAGACTGCGACTCGCCCTGTCGCGCGTCC 448
Db 872 CCTAGGGGAAAGCTGTTGCTGTCGTCGCAAGCTGCGACACACGGGCTTCTGCGCTGCT 931
QY 449 TGCTGAAGSAGAGTACCAGCCCAAGGCGCAGTTTCAACCAAGGCCAAGTCTGCTGCTA 508
Db 932 ACCTCAAGAGCACTTACCAGTCCATGTCATCTACGACGCGCAAGTGGCTTCTGCA 991
QY 509 TCCACAACATCGCTTCCAGGCGCGCATGTGSGGAGGCTTTCAGGACACGAAGCTGC 568
Db 992 TCCACAACATCTGCTACAGGCGCGCTTCTCTTCGAGGACTTTCGCGAGCTCAACCTGC 1051
QY 569 CCGAGCGCGCTTTCAGAACTGCGCTTCTCGGACGCGTATGCAAGGTTTACACTGAGG 628
Db 1052 CCGACAGGTTCAAGTCTGCTTCTGACTTCAATTGACGGCTACGACAAAG----- 1098
QY 629 CCACCCCATGAGGAGGACGAGAGAGCCCGCTGACGGGAAGACCTTACAAGAAGATCA 688
Db 1099 -----CCGCTGAGGGGGCG-----AGATCA 1120
QY 689 ACTGCTGAAGGTTGCTATTCGCGCGCGACAAAGCTGCTGACTGTGCGCCCACTAGG 748
Db 1121 ACTGATGAAGCGCGGATCTGCGAGCGGCAAGGCTGCTGAGCTGAGCGCCCTACTAGG 1180
QY 749 CGACCGAGATCGCTGCGATGCGCGCGGGGTGTGAGCTGACACACCGCTCATCCGGCCA 808
Db 1181 CTGAGGAGCTATCTCTGCGAAGCGAGGCGGTGCGAGCTGACACATCATCGCGCTCA 1240
QY 809 AGGCACTGAGGCACTGTGAAGCGCATGGACATTGAGGAGTGGAAACCCCAAGACCGACA 868
Db 1241 CGGGATACCGGAATCGTCAACGCGATGGAGCTGAGTGGAGTGGACCCCAAGGACA 1300
QY 869 AGTTCCTGCTGCTGCGCCCTACGACCAAGAGCTCTACCGCGCAAGGCGCGCGCAAGG 928
Db 1301 AGTTCCTGCGCTCACTACGACATCACCAACCGGCTTGGAGGCAAGGCGCTGAACAAGG 1360
QY 929 AGGCGCTGAGCGGCTGAGGCGCTGCTGAGACCCACCGCGCCCTGCTGCGCTTCA 988
Db 1361 AGGCGCTGAGCGGCTGAGGCGCTGCTGAGGAGGAGTGGCGCTGAGGCGCTTCA 1420
QY 989 TCGGCGCTGAGGAGCAAGAGGCTGTCATCATCTGCGCGCGCCGCGCCCAAGATCC 1048
Db 1421 TCGGAGGCTGAGGAGCAAGAGGCGCGCGATGATGATGCGCGCCATCCCGGAGATCC 1480
QY 1049 TGGCCACCCCAAGGTGCGATCGGCATCTCTGGGTACCGGCAAGCGCGCTACGAGAAGC 1108
Db 1481 TGAAGGAGGAGGAGCTGCGAGATCTCTCTTGGCACCGGGAAGAGAGTITGAGAAGC 1540
QY 1109 TGGTGAAGCGCATCGCACCAAGTACAAGCGCGCGCCCAAGGCGGTGCTCAAGTCTCGG 1168
Db 1541 TGTCAAGAGCATGAGGAGAGAGTTCCTCCCGGCAAGGTGAGGCGGTGCTGAGTCTCAAG 1600
QY 1169 CGCCCTGCGGACATGCTCAACCGCGCGCGGAGCTTCACTGCTGCTGCTGCGCTGCTG 1228
Db 1601 CGCCGCTAGCTCACCAGATGATGCGCGCGCGGAGCTTCTGCTGCTGCTCACCAGCGCTG 1660

QY 1229 AGCCCTGCGGCTGATCCAGCTGACGCGCATGCACTACGTTACCGTCCCGCTGGTAGCCT 1288
Db 1661 AGCCCTGCGGCTCCTCAGCTGATGCGGAAATGCTATGGAACGCGCTGCTGCGGCT 1720
QY 1289 CCACGGGCGGCTGCTGACACCGCTCAAGGAGGGGCTCACCGGCTTCCACATGGCGGCC 1348
Db 1721 CCACGGGCGGCTGCTGACACCGCTGCTGAGGGGCAAGACCGGGTTCACATGGCGGCC 1780
QY 1349 TGA-----ACCCCGACAAAGCTGGACGAGCTGACGCGCGACCGCTGCGCGCCACCGTGC 1402
Db 1781 TCAGGCTGACTGCAACGCTGCTGAGCGCGCGAGCTGAAGAAGCTGGCGACACCTCA 1840
QY 1403 GCGGTGCGACGAGTGTTCGCGCGCGGCTACCCCGAGATGCTGGCCACTGCATCA 1462
Db 1841 AGCGGGCGTCAAGCTCGTCGCGACGCGCGCTACGAGGATGCTCAAGAATGCATGA 1900
QY 1463 GCCAGACTGCTCTGCTGCTCAAGCGCGCGCAAGTGGAGGCGCTGCTGGAGGAGTGG 1522
Db 1901 TCCAGATCTCTCTGGAAGGACCTGCAAGAATGGAGGAGCTGCTTCTGGAAGTGG 1960
QY 1523 TGTACGCGAAGGCGCGCTGCGCACCGCGCAAGAGAG 1560
Db 1961 GGTGGAGGAGCGAGCGCGGATCGTCGCGGAGGAG 1998

RESULT 11
AF486515 1827 bp mRNA linear PJN 02-JUL-2002
LOCUS Hordeum vulgare cultivar waxy oderbrucker granule bound starch
DEFINITION Synthese I mRNA, complete cds.
ACCESSION AF486515
VERSION AF486515.1 GI:21667429
KEYWORDS
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1827)
AUTHORS Patron,N., Smith,A., Fahy,B., Hylton,C., Naldrett,M., Rossnagel,B.
and Denyer,K.
A mutation in the 5' non-coding region of the barley GBSSI gene
alters its temporal and spatial expression and reduces GBSSI
activity and amylose content in the endosperm
Unpublished
Patron,N.
Direct Submission
Submitted (22-FEB-2002) Metabolic Biology, John Innes Centre,
Norwich Science Park, Norwich, Norfolk NR4 7UH, UK
LOCATION/Qualifiers
1. .1827
/organism="Hordeum vulgare"
/cultivar="waxy oderbrucker"
/db_xref="taxon:4513"
1. .1827
/note="alpha glycosyl transferase"
/codon_start=1
/product="granule bound starch synthase 1"
/protein_id="AAM74049.1"
/db_xref="GI:21667430"
/translation="MAAATLSQIA*SGTVLGYDTRAPSMEFHAGFOGLRPRKPADGT
FQMRIVGASAPKQSKAHNRGLSVVVRATGSGMNLVFGAEPAPKSKTGGLDV
LGGLPPAMAANGHRVMVSPRYDQKADMTSVISEIKVADETERVRFPHCKRGVDR
VFIDHPLEKVRGKTKERYDQADGTEDNOQRFSLCOALRAPRLINLNINNYF
SPGYDVFVVCNDWHTGLLACYLAKSNYGLYRTAKVFCIHNISYQGRSFDFFA
QNLNDRKSSDFIDYDKPVEKRIKNNKAGILQADKVLTVSPYIAELISGEARG
CELDNMLRLTGTITLVNGQDVSEWPTDKFLAVNYDITTALEAKALKEALQAEVGL
PVDKVPVAFVIGRLEQKQDPMIAIPEILKEEDVQIILLCTGKFKFKLLKSMEE
KFPKVRVAVRFNAPLAHOMAGADIIATSRFECGLIQLOLMRGTGTCVCASTGGL
VPTIVGKTGHMGLSDVNCVNPADKKVATTLKRVKVVGTGPAYQEMKNCMTQD
LSWKFPKKNWEDVLLLELGVGSEPGIVGEIAPLAMEVAAAP"

CDS
1. .1827
/note="alpha glycosyl transferase"
/codon_start=1
/product="granule bound starch synthase 1"
/protein_id="AAM74049.1"
/db_xref="GI:21667430"
/translation="MAAATLSQIA*SGTVLGYDTRAPSMEFHAGFOGLRPRKPADGT
FQMRIVGASAPKQSKAHNRGLSVVVRATGSGMNLVFGAEPAPKSKTGGLDV
LGGLPPAMAANGHRVMVSPRYDQKADMTSVISEIKVADETERVRFPHCKRGVDR
VFIDHPLEKVRGKTKERYDQADGTEDNOQRFSLCOALRAPRLINLNINNYF
SPGYDVFVVCNDWHTGLLACYLAKSNYGLYRTAKVFCIHNISYQGRSFDFFA
QNLNDRKSSDFIDYDKPVEKRIKNNKAGILQADKVLTVSPYIAELISGEARG
CELDNMLRLTGTITLVNGQDVSEWPTDKFLAVNYDITTALEAKALKEALQAEVGL
PVDKVPVAFVIGRLEQKQDPMIAIPEILKEEDVQIILLCTGKFKFKLLKSMEE
KFPKVRVAVRFNAPLAHOMAGADIIATSRFECGLIQLOLMRGTGTCVCASTGGL
VPTIVGKTGHMGLSDVNCVNPADKKVATTLKRVKVVGTGPAYQEMKNCMTQD
LSWKFPKKNWEDVLLLELGVGSEPGIVGEIAPLAMEVAAAP"

FEATURES
source

BASE COUNT 364 a 567 c 294 t

ORIGIN

Query Match 33.2%; Score 528.4; DB 8; Length 1827;
Best Local Similarity 61.6%; Pred. No. 1.7e-49;
Matches 984; Conservative 0; Mismatches 521; Indels 93; Gaps 5;

QY 5 TGGACATCGTGTGCTGCTGAGTCCGCCCTTGGTCCAGAGAGGGGGCTGGGG 64
DB 242 TGNACCTCGTGTTCGTCGGCGCGAGATGGCGCTTGGAGACCGGGCGCTTGGG 301

QY 65 ATGTGACTGGTGGCCCTGCTATTGAGCTGTCAAGCGCGCCACCGCGTCATGACCATG 124
DB 302 ACCTCTCGGGGSCCTTCCACAGCCATGGCCGCCAAGGTCACCGGGTGATGCTGTCT 361

QY 125 CCCCTCGTACGACAGTACGCTGACCGCTGGGACACCTCGGTGGTGGACATATGG 184
DB 362 CCCCGGCTACGATCAGTACAGGACCGCTGGGACACCGCTCATCTCGGAGTCAAGG 421

QY 185 -----CGGAGAAGGTCCTGCTTCCACTCCATCAAGAGGGCGTGCACCGG 232
DB 422 TCGCTACGAGTACGAGAGGTTGAGTCTTCCACTGCTACAGCGCGAGTGGACCGG 481

QY 233 TGTGGATTGACCAACCCCTGTTCTTGGCCAAAGTCTTGGGCAAGACCGGCTCCAAAGCTGT 292
DB 482 TGTTCATGACCAACCCCTGTTCTTGGAGAAGTCTCGGGGCAAGACCAAGGAGAATCT 541

QY 293 ACGGCCCGCTCCGCGCTGACTACTGACCAACCAAGCGCTTCGCGCTGTTCTGCA 352
DB 542 ACGGCCCGGACCGCGGCTAGGAGGCAACCAAGCGCTTCAGCGCTTCTCTGCG 601

QY 353 AGCGCGCTATTGAGGTCGCCGCTGCTGCCCTTC -----G 388
DB 602 AGGACGCTCGAGGACCCAGGATCTCAACTCAACAAACCCCTACTTTTCGGTC 661

QY 389 GCGCGCGGAGGACGCTGCTTCTGTCGCAACGACTGGCACTCCGCCCTGTCGCCGTC 448
DB 662 CTACGGGGAAGACGCTGCTGCTGCAACGACTGGCACACGCGCTTCGGCTGCT 721

QY 449 TCTGAAGGACGACTACGAGCCAGGCGCAGTTTACCAAGGCGCAAGTGGTGGCTA 508
DB 722 ACTCAAGAGCACTACCAAGTCCATGCGCATCTACAGGACGCGCAAGTGGCTTCTGCA 781

QY 509 TCCCAACATCGCTTCCAGGCGCGCATGTGGAGGAGCTTTCAAGGACACGAGCTCG 568
DB 782 TCCCAACATCTGTAACAGGCGCTTCTCTCTGACGACTTGGCGAGCTCAACCTCG 841

QY 569 CCCAGCGCGCTTGAAGAGTGGCTTCTCGGACGGCTATGCCAAGGTTTACACTGAGG 628
DB 842 CCGACAGGTTCAAGTCTGCTTCGACTTCATTGACGGCTTAACGACG ----- 888

QY 629 CCACCCCATGAGGAGGACGAGAGCCCGCTGACGGGAAGACCTACAGAGATCA 588
DB 889 -----CCGCTGAGGGGCGC -----AAGATCA 910

QY 689 ACTGCTGAAGGTTGGCATTAATGCGCGCGCACAAAGTGGTACTGTGTCGCCCACTAG 748
DB 911 ACTGATGAAGGCGCGGATCTGCGAGGCGCAAGGCTGCTGAGCTGAGCCCTACTAG 970

QY 749 CCACGAGATCGCTCGCATGCCGCGCGGGGTGTGAGCTGACACCGGTCATCCGCGCA 808
DB 971 CTGAGGAGCTCACTCTGCGGAAGCGAGGGCTGGGCTGCAACATCATGCGCTCA 1030

QY 809 AGGCGATTGAGGCGCTTGTGAACGCTGACATTTGAGAGTGAACCCCAAGACCGCA 868
DB 1031 CGGGATCACCAGATCTCAACGGCTAGGAGTCAAGTGGAGCGGACCCCAAGAGCA 1090

QY 869 AGTTCCTGTCGCGCTTACGACCAAGACAGGCTTACCGCGGCAAGCGCGCGCAAGG 928
DB 1091 AGTTCCTGCGCTCAACTACGACATCAACACCGCTTGGAGCGCAAGCGCTGACAAAG 1150

QY 929 AGGCGCTGACGCGGCTGCGCTGTTGGACCCACCGCGCGCGCTGTCGCTTCA 988
DB 1151 AGGCACTGACGCGGAGTGGGGCTGCGCGTGGACAGGAAGTGGCGCTGGTGGCTTCA 1210

QY 989 TCGCCGCTGGAGGACAGAGGTTGTGGACATCATCTTGGCGCGCTGCCAAGATCC 1048
DB 1211 TCGCAGGCTGGAGGACAGAGGCGCCGACGTGATGATCGCCGCTATCCGGAGATCC 1270

QY 1049 TGGCCACCCCAAGGTGAGATGCCATCTTGGTACCGCAAGCGCGCTTACGAGAAGC 1108
DB 1271 TGAAGGAGGAGGACGTCAGATCATCTCTTGGCACCGGGAAGAGATTTGAGAAGC 1330

QY 1109 TGTGTACGCGCATCGGACCAAGTACAGAGGCGCGCCCAAGGCGCTGCTCAAGTCTCGG 1168
DB 1331 TGTCTAAGACATGGAGGAGAAGTTCCCGGGCAAGGTGAGGCGCGCTGCTCAGGTTCAACG 1390

QY 1169 CGCCCTTGGCGGCATGCTCACCGCGCGCGCTTCACTGCTGCTGCCCTCGCGCTCG 1228
DB 1391 CGCGCTAGCTACCATGATGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1450

QY 1229 AGCCCTGCGGCTGATCCAGCTGACGCCATGACCTACGTTACGTTACGTTACGTTACG 1288
DB 1451 AGCCCTGCGGCTTCACTGACGCTGAGGAAATGCGCTATGGAAGCGCGCTGCTGCTG 1510

QY 1289 CCACCGCGCGCTGCTGACACCGTCAAGGAGGCGCTCACCGCTTCCACATGGCGGCC 1348
DB 1511 CCACCGCGCGCTGCTGACACCGTCAAGGAGGCGCTCACCGCTTCCACATGGCGGCC 1370

QY 1349 TGA-----ACCCGCAACGCTGAGGAGGCTGACGCGGACGCGCTGGCGCGCACCGCTGC 1402
DB 1571 TCAGCGTGGACTGCAACGCTGTTGGAGCGCGGACGTGAAGAGGTGGCGCACCTGA 1630

QY 1403 GCGTGGCAGGAGTGTGTTGGCGGCGCGCTACCCGAGATGGTGGCGCACTGATCA 1462
DB 1631 AGCGCGCGCTCAAGGCTGTCGCGCACGCGCGCTTACAGGAGATGGTCAAGACTGATGA 1690

QY 1463 GCAGGACCTGCTCTGCTTCAAGCGCGCCAGAGTGGAGGCGCTGCTGGAGAGTGG 1522
DB 1691 TCCAGATCTCTCTGAGGAGGACCTGCCAAGACTGGGAGGAGCTGCTTGGAACTGG 1750

QY 1523 TGTACGCGAGGCGCGCTGGCGCCACCGCGCAAGAGGAG 1560
DB 1751 GGTGGAGGAGGAGCGCGGATGCTGGCGGAGGAG 1788

RESULT 12

AF486518 1827 bp mRNA linear PLN 02-JUL-2002
LOCUS Hordeum vulgare cultivar SB 85750 granule bound starch synthase I
DEFINITION mRNA, complete cds.
ACCESSION AF486518
VERSION AF486518.1 GI:21667435
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1827)
AUTHORS Patron,N., Smith,A., Fahy,B., Hylton,C., Naldrett,M., Rossnagel,B.
and Denyer,K.
TITLE A mutation in the 5' non-coding region of the barley GBSSI gene alters its temporal and spatial expression and reduces GBSSI activity and amylose content in the endosperm
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1827)
AUTHORS Patron,N.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Metabolic Biology, John Innes Centre,
Norwich Science Park, Norwich, Norfolk NR4 7UH, UK
FEATURES
source
location/Qualifiers
1..1827
/organism="Hordeum vulgare"
/cultivar="SB 85750"
/db_xref="taxon:4513"
1..1827
CDS

AUTHORS Patron, N., Smith, A., Faby, B., Hylton, C., Naldrett, M., Rosnagel, B. and Denyer, K.
TITLE A mutation in the 5' non-coding region of the barley GBS1 gene alters its temporal and spatial expression and reduces GBS1 activity and amylose content in the endosperm
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1812)
AUTHORS Patron, N.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Metabolic Biology, John Innes Centre, Norwich Science Park, Norwich, Norfolk NR4 7UH, UK
FEATURES
source Location/Qualifiers
1..1812
/organism="Hordeum vulgare"
/cultivar="CDC Alamo"
/db_xref="taxon:4513"
1..1812
/note="alpha glucosyl transferase"
/codon_start=1
/product="granule bound starch synthase I"
/protein_id="AA074052.1"
/db_xref="GI:21667438"
translation="MAALATSLATSGTIVLGTDRFRPFQGLRPNPADAALGMRTIGASAPKQSRKHSRRCLSVVVSATGSGMNVFVGAEMAPWSKTGLGLVGLSLP
PAMAAGHRVWVSPRYDQYKDAWTSVISELKVADEVREVRFEHCYKRGVDRVIDH
PWFLEKVRKTEKIXYGPAGTDIEDNQRFSLLCOALEAPRILNLRNPNPFSGPG
EDVVFVNDHHTGLACILKSNYISNGIYRTAKVAFCHNISYQGRFSDFDAQNLPL
DRFKSDFIVGYDRPEVGRKINMKAGILQADKLVTSYIAEELISGEARGCELDN
IMRLFGITVINGMDVSDWPTKDFLAVNYDITALEAKLNKLEALQAEVGLPVDK
VPLVAFIGRLQKQPDVMIAPILKEEDVOIILGLTGKKKLEKLKLSMEKPPGK
VRVVFENAPLHOMMAGADLLAVTSREPCGLIOLOGMRYGTPOCVASTGLVDLIV
EGKTFGRMLSDCNVPEADVPKAVATILKRVKVVVTPAQEMVKNVCVVDLSWKG
PAKNEDVLLLELGVSGSEPGIVGEIEIPLAMENVAAP"
BASE COUNT 359 a 565 c 599 g 289 t
ORIGIN
Query Match 33.0%; Score 525.2; DB 8; Length 1812;
Best Local Similarity 61.5%; Pred. No. 3.9e-49;
Matches 982; Conservative 0; Mismatches 523; Indels 93; Gaps 5;
QY 5 TGGACATCGTGATGGTGTGCTGAGTGCCTTGGTCCAAAGCGGCGGCTGGCG 64
DB 227 TGAACCTCGTGTGCTGCGCGGAGATGGCGCTTGGAGCAAGACGCGGCTGGCG 286
QY 65 ATGTGACTGTCGCTTCCTATGACTGTGAAGCGGCGGCGGCTGATGACCATG 124
DB 287 ATGTCTCGGCGGCTTCCTCGGCGGATGGCGGCGGCGGCTGATGCTGCT 346
QY 125 CCCTCGCTACGACAGTACGCTGAGCGCTGGGACACCTCGGTGCTGGACATG 184
DB 347 CCGCGGCTACGATCAGTACAGGAGCGCTGGGACACCGGCTGCTCGGATCAAG 406
QY 185 -----GCGAGAGTCCGCTACTTCCACTCCATCCAAAGAGCGGTGCACCG 232
DB 407 TCGTGACGAGTACGAGAGGTGAGGTCTTCCACTGCTACAAAGCGGAGTGGACCG 466
QY 233 TGTGATTCACCACTTCCTGCTGGCAAGGTCTGGGCGGAGACCGGCTCCAACTGT 292
DB 467 TGTTCATCACCACCGCTGCTTGGAGAGGTCTCGGCGGCAAGAGTCCAAAGAGATCT 526
QY 293 ACGGCGCGGCTCGGCGCTGACTACTGACAAACACAAAGCGCTCGGCTGCTTGTGCA 352
DB 527 ACGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 586
QY 353 ACGGCGCTATTGAGGCTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 388
DB 587 AGGAGCACTCGAGGCAACCGGATCTCACTCAACACACACACCTTCTTGTGCT 646
QY 389 GCCCGGCGGAGGACTCGCTTCTGCTGGCGGCAAGACTGCGGCGGCTGCGGCGGCT 448
DB 647 CTAAGGGAAGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
QY 449 TGTGAGGAGGAGTACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 508

Db 707 ACCTCAAGACCACTTACAGTCCAAATGGCATCTACAGAGCGGCGGCGGCTTCTGCA 766
QY 509 TCACACATCGCTTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 568
Db 767 TCACACATCTCGTACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 826
QY 569 CCCAGGCGGCGCTTTGACAAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 628
Db 827 CCGACAGGTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 873
QY 629 CCACCCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 688
Db 874 -----CCGCTGGAGGGCGC-----AAGATCA 895
QY 689 ACTGGCTGAAGGTGGCATTTATCGCGCGGACAGCTGGTACTGTCTGCGCCCACTACG 748
Db 896 ACTGGATGAAGCGGCGGATCTCGAGCGCGGAGAGGTGCTGAGGCGGCGGCGGCTTACTACG 955
QY 749 CGACCGAGATCGCTGCGCGATGCCCGCGGCGGCTGTGAGCTGGACACCGCTCATCGCGCCA 808
Db 956 CTGAGGAGCTCATCTCTGGCGAAGCCAGGCGCTGCGAGCTCGACACATCATGCGGCTCA 1015
QY 809 AGGCGATTGAGGCGATTGTGAAGCGGATGACATTTAGGAGTGGAGCCCAAGACCGACA 868
Db 1016 CGGGGATCACCGGAATCGTCAACGGCATGACGCTGAGTGGAGGCGGCGGCGGCGGCG 1075
QY 869 AGTTCTCTGCTGCGCGCTACGACAGCAAGCGTCTACGCGGCGGCGGCGGCGGCGG 928
Db 1076 AGTTCTCTGCGCTCACTAGCATATCACCGCGCTTGGAGGCGGCGGCGGCGGCTGAGCAAG 1135
QY 929 AGCGCTTGCAGGCGGCTGCGCTGCTGAGACCGGCGGCGGCGGCGGCGGCGGCGGCTG 988
Db 1136 AGCGCTTGCAGGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1195
QY 989 TCGCGCGCTGGAGGAGCAGAGGCTGTGACATCATCTTGGCGGCGGCGGCGGCGGCGG 1048
Db 1196 TCGGAGGCTGGAGGAGCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1255
QY 1049 TGGCGCACCCCAAGTGCAGATCGCATCTCTGGGTACCGCAAGCGGCGGCGGCTACGAGAGC 1108
Db 1256 TGAAGGAGGAGGAGCTCCAGATCATCTCTTGGCACCGGAGAGAGAGAGAGAGAG 1315
QY 1109 TGTGTACGCCATCGGCGCACCAAGTACAAAGGCGGCGGCGGCGGCGGCGGCGGCGG 1168
Db 1316 TGTCTAAGACATGAGGAGAGAGTTCGCGGCAAGGTGAGGCGGCGGCTGCTCAGGTTCAAG 1375
QY 1169 CGCGCTTGGCGGCGATGCTCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1228
Db 1376 CGCGCTTAGCTACCAAGATGATGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1435
QY 1229 AGCGCTTGGCGGCTGATCCAGCTGACGCGCATACGCTACGCTGCGGCGGCGGCTGAGCCT 1288
Db 1436 AGCGCTTGGCGGCTTACCGCTCCAGGAGTGGCTATGGAACGCGGCTGCTGCGGCT 1495
QY 1289 CCACCGGCGGCTTGTGCGACACCGTCAAGAGGCGGCTGACCGGCTTCCATATGGGCGGCG 1348
Db 1496 CCACCGGCGGCTTGTGCGACACCGTCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 1555
QY 1349 TGA-----ACCGCGGAGCTGAGGAGCTGACCGCGGCGGCGGCGGCGGCGGCGGCTG 1402
Db 1556 TCAGCTGCTACTCAAGCTGGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1615
QY 1403 GCGCTGCCAGGAGGTGTTTGGGCGGCGGCTACCGCGAGATGGTGGCGGCGGCGGCTG 1462
Db 1616 AGCGGCGGCTCAAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1575
QY 1463 GCGAGGAGCTGCTCTGCTTCCAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1522
Db 1676 TCCAGGATCTCTCTGGAAGGAGCTGCCAAGAACTGGGAGGAGCTGCTCTGGAAGCTG 1735
QY 1523 TGTACGGAAGGCGGCGGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1560

Db 1736 GGTGGAGGGAGGAGCCGGGGATCGCGCGAGGAG 1773

RESULT 14
AF486516 1827 bp mRNA linear PLN 02-JUL-2002
LOCUS Hordeum vulgare cultivar Von M Kei non-functional granule bound
DEFINITION starch synthase I, complete sequence.
ACCESSION AF486516
VERSION AF486516.1 GI:21667431
KEYWORDS
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1827)
AUTHORS Patron,N., Smith,A., Fahy,B., Hylton,C., Nalderett,M., Rosnagel,B.
and Denyer,K.
TITLE A mutation in the 5' non-coding region of the barley GBSSI gene
alters its temporal and spatial expression and reduces GBSSI
activity and amylose content in the endosperm
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1827)
AUTHORS Patron,N.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Metabolic Biology, John Innes Centre,
Norwich Science Park, Norwich, Norfolk NR4 7UH, UK
FEATURES
source
1..1827
/organism="Hordeum vulgare"
/cultivar="Von M Kei"
/db_xref="taxon:4513"
misc_feature
1..1827
/note="contains non-functional granule bound starch
synthase I due to premature stop codon"
BASE COUNT 364 a 565 c 601 g 297 t
ORIGIN
Query Match 33.0%; Score 525.2; DB 8; Length 1827;
Best Local Similarity 61.5%; Pred No. 3.9e-49;
Matches 982; Conservative 0; Mismatches 523; Indels 93; Gaps 5;
QY 5 TGGACATCGTATGTTGTGTGAGTGGCGCCCTGTGTCACAGAGGGCGCGCTGGGG 64
Db 242 TGAACCTCGTGTGTCGGCGCGAGATGGCGCCCTGGAGCAAGCCGCGCGCTTGGGG 301
QY 65 ATGTGACTGGTGGCTGCTATTAGCTGTGTCAGCGCGCGCCACCGCGTCATGACCAT 124
Db 302 ACGTCTCGCGCGCTTCCACAGCATATGGCGCCGCAACCGGTACCGGGTGATGGTGGT 361
QY 125 CCCCTCGTACACAGTACGCTGAGCGCTGGGACACCTCGGTGTCGTGGACATCATGG 184
Db 362 CCCCAGCTACCATGATACAGGAGCGCTGGACACCGCTCATCCGAGATCAAGS 421
QY 185 -----GCAGAGGTCGGTACTTCGACTCCATCAAGAGAGGCGTGCACCGG 232
Db 422 TCGCTGACAGTACGAGGAGTGGTTCCTCCACTGCTACAGCGCGAGTGGACCGG 481
QY 233 TGTGATTGACACACCTGTTCTGTCGCAAGTCTGGGCAAGACCGGCTCCAGCTGT 292
Db 482 TGTTCATGACACCGCTGTTCTTGAGAGAGTTCGGGCAAGACCAAGGAGAGATCT 541
QY 293 ACGGCCCCCGCTCGGCGCTGACTACCTGGACACCAAGAGCGCTTCGCCCTGTTCTGCA 352
Db 542 ACGGCCCCAGCGCGACGGACTACGAGGACCAACAGTAGCGCTTCAGCCTTCTCTGCC 601
QY 353 AGCGCGCTATTGAGCTGCGCGTGTCTGCTTC-----G 388
Db 602 AGGCGCTCGAGGACCGCCAGGATCTCAACCTCAACACCAACCCCTACTTTCTGGTC 661
QY 389 GCGCGCGGAGGACTCGCTTCGTTGGCCACAGTGGCACTCGCGCTGTGGCGCTGCC 448

Db 662 CCTACGGGGAAGACGTGGTGTTCGTGTCAACAGACTGGCACGGGCTTCTTCGCGCTGCT 721
QY 449 TGCTGAAGACGAGTACCAGCCCAAGGCCAGTTCACCAAGGCCAAGTCCGGTCTGGCTA 508
Db 722 ACTCAAGAGCAACTACCAAGTCCATATGGCATCTACAGGAGCGCCCAAGGTGGCCTTCTGCA 781
QY 509 TCCACAACATCGCTTCCAGGCGCGCATGTGGGAGGAGGCTTTTCAAGGACACGAACTGC 568
Db 782 TCCACAACATCTCGTACCAGGCGCGCTTCTCTTCACGACCTTTCGCGAGCTCAACCTGC 841
QY 569 CCGAGCGCGCTTGTACAAGCTGGCGCTTCTCGGACCGCTATGCCAAGGTTTACACTGAGG 628
Db 842 CGACAGGTTCAAGTCTGCTCTTCGACTTTCATTTGACCGCTACGACAAG----- 888
QY 629 CCACCCCATGAGGAGGAGGAGAGAGAGCCCGCTGACGGGAAAGACCTACAAGAAGATCA 688
Db 889 -----CCCTGGAGGGGCGC-----AAGATCA 910
QY 689 ACTGCTGAAGGTTGGCATATTATGCGCGCGACAAAGTGTGTGACTGTGCGCCCACTACG 748
Db 911 ACTGGATGAAGCGCGGATCTGACGGCGGACAAAGTGTGTGAGCTGAGCCCTACTACG 970
QY 749 CGACCGAGATCGTCCGATGCGCGCGGTGTGTGAGCTGGACCGCTCATCCGCGCA 808
Db 971 CTGAGGAGCTCATCTCTGGCAAGCCAGGGGTGCGAGCTTCGACAACATCATCGGCTCA 1030
QY 809 AGGGCATGAGGCAATGTCAACGGCATGGACATTTGAGGAGTGAACCCCAAGACCGACA 868
Db 1031 CGGGATCACCGAATCGTCAACGGCATGAGCTGAGTGGAGCCCGCCACCAAGACA 1090
QY 869 AGTTCTGTGTGCGCTTACGACCAAGACAGCTCTACGCGCGCAAGGCGCGCGCAAGG 928
Db 1091 AGTTCTGTGCGCTCAACTACGACATCACACCGCTTGGAGGCAAGGGCTGAACAAGG 1150
QY 929 AGSCCTGTCAGCGCGAGCTGGGCTGCTGTGACCCCAACCGCCCTTCTTTCGCTTCA 988
Db 1151 AGGACTGCGCGGAGGTGGGCTGCGGTGGACTTGGAGTGGCGCTGGTGGCGCTTCA 1210
QY 989 TGGCGCGCTGGAGGAGCAGAGGTTGTGACATCATCTGCGCGCGCTTCCCAAGATCC 1048
Db 1211 TCGGAGGCTGGAGGAGCAGAGGCGCGCGCTGATGATCGCGCTATCCCGGAGATCC 1270
QY 1049 TGGCCACCCCAAGGTGAGATCGCATCTCTGGTACCGGCAAGGCGCTTACGAGAAGC 1108
Db 1271 TGAAGAGGAGGAGCTCCAGATCATCTCTTGGCAACCGGAGAGAAAGTTTGAAGC 1330
QY 1109 TGGTGAACGCTATCGGCACCAAGTCAAGGCGCGCGCAAGGCGGTGCTCAAGTTCGG 1168
Db 1331 TGCTCAAGAGCATGGAGGAGAGTTCGCGGCAAGGTGAGGCGCTGGTCAAGTCAAGC 1390
QY 1169 CGCCCTGGCGCATCTGCTACCGCGCGCGCGCTCATGCTGCTGCTGCGCTGCTG 1228
Db 1391 CGCGCTAGCTACACAGATGATGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1450
QY 1229 AGCCCTGCGGCTGATCCAGCTGACGCGCATGCTACGTCACGTCGCGCTGCTGCTG 1288
Db 1451 AGCCCTGCGGCTGATCCAGCTGACGCGCATGCTACGTCACGTCGCGCTGCTGCTG 1510
QY 1289 CCACCGCGCGCTTGTGTCACACCGCTCAAGGAGGCGCTTCCAGGCTTCCAGTGGCGCC 1348
Db 1511 CCACCGCGGCTGCTGTCACACCGCTGTCAGGAGGAGAGTGGTTCACATGGCGCC 1570
QY 1349 TGA-----ACCCGCAAGCTGGAGAGGCTCACCGCGAGCGCTTGGCGCCACCGTGC 1402
Db 1571 TCAGCGCTGACTCAACAGTGGTGGAGCGCGGACCTGAAGAAGTGGCGGACCCCTGA 1630
QY 1403 GCGTCCAGGAGGAGTGGTGGCGGCGGCTACCCCGAGATGGTGGCGCACTGATCA 1462
Db 1631 AGCGGCGCTCAAGGTCGTGGCACCGCGCTACCAAGGAGTGGTCAACAACATGATGA 1690
QY 1463 GCGAGGCTGCTGCTGCTCAAGCGCGCGCGCTGAGGAGGCTGCTGAGGAGGAGTGG 1522
Db 1691 TCCAGGATCTCTCTGGAAGGAGCTGCCAAGAAGCTGGGAGGAGGCTGCTTCTGGAAGTGG 1750


```
QY 1523 TGTACGGCAAGCGCGGTGGCCACCGCCCAAGAGAG 1560
Db 1751 GGGTGGAGGGGAGCGAGCGGGGATCGTCTGGCGGAGAG 1788

RESULT 15
AF486517
LOCUS AF486517 1827 bp mRNA linear PLN 02-JUL-2002
DEFINITION Hordeum vulgare cultivar Iyatoma Mochi granule bound starch
synthase I mRNA, complete cds.
ACCESSION AF486517
VERSION AF486517.1 GI:21667433
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1827)
AUTHORS Patron,N., Smith,A., Fahy,B., Hylton,C., Naldrett,M., Rossmagel,B.
and Denyer,K.
TITLE A mutation in the 5'-non-coding region of the barley GBSSI gene
alters its temporal and spatial expression and reduces GBSSI
activity and amylose content in the endosperm
JOURNAL Unpublished
AUTHORS Patron,N.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2002) Metabolic Biology, John Innes Centre,
Norwich Science Park, Norwich, Norfolk NR4 7UH, UK
FEATURES
source
1..1827
/organism="Hordeum vulgare"
/cultivar="Iyatoma Mochi"
/db_xref="taxon:4513"
1..1827
/note="alpha glucosyl transferase"
/codon_start=1
/product="granule bound starch synthase I"
/protein_id="AA074050.1"
/db_xref="GI:21667433"
1..1827
/translation="MAALATSQLATSGTLVGTVDORSAPMFHAFQGLRPKPADGT
FGMTVGASAPKSRVRAHNRKLSVVRATGSGMNVFVGAEMAPWSKTLGLGDV
LGGLPAMANGHVMVSPRYDQIKDAWDSVISEIKVADEYEVRFHCYKRGVDR
VFIDHPFLERVKRTEKIKYDPDAGDYEDNQRFSLCQAALAPRILNINNPYF
SGPYGDFVFNDRWHTGLACLYLSNYSNGIYRTAKVAFCHINISYOGFSPDFA
QLNLPDRFKSDFIDYDKFVEGRKINWKAGILOAKVLTVPYAEELISGEARG
CELDNIMRLTGITGVNMDVSEMDPTKDFLAVNYDITTALEKALNKEALQEVGL
PVDKVPVAVFAPLAHOMMAGADILLAVTSRFEPCGLIQGMRYGTPVCVASTGGL
VFIVGKTFHMRGLSDVNCNVPEADVKVATTLKRAVKVVGTPAYOEMYNKMIQD
LSWKGPAKNMEDVLLLELGVESGSEPIVGEETAPLAVENVAAP"
BASE COUNT 364 a 566 c 601 g 296 t
ORIGIN

Query Match 33.0%; Score 525.2; DB 8; Length 1827;
Best Local Similarity 61.5%; Pred. No. 3.9e-49;
Matches 982; Conservative 0; Mismatches 523; Indels 93; Gaps 5;

QY 5 TGGACATCGTGTGCTGCTAGGTGCGCCCTGTGTCACAGACGGCGGCGCTGGCG 64
Db 242 TCAACTCGTGTCTCGCGCGGAGATGGCCCTCGGAGCAGACCGCGGCGCTGGCG 301
QY 65 ATGTGACTGTGGCTGCTATTGAGTGTGTAAGCGCGGCCACCGCGTCAATGACATG 124
Db 302 ACCTCTCGCGCGCTTCCACCGCATGCGGCCAACGGTCACGGGTGATGTCGTCT 361
QY 125 CCCCTCGTAGCAGCATAGCTACGCTCGGACACCTCGGTGTGTCGACATCATGG 184
Db 362 CCCCGCGCTACGATACAGAGGACGCGCTGGACACCGGCTATCTCCGAGATCAAG 421
QY 185 -----GCAGAGAGTCCGCTACTTCCACTCCATCAAGAGAGGGCGTGCACCGCG 232
```

```
Db 422 TCCTGACGAGTACGAGAGGGTGAAGTTCTTCCACTGCTACAAAGCGGAGTGAACGCG 481
QY 233 TGTGGATTGACCACCCCTGTTCTCTGTCGAAGGTCTGGGCAAGACCGGCTCAAGCTGT 292
Db 482 TGTTCATCGACCACCCGCTGTTCTTGGAGAAAGTTCGGGGCAAGCAAGAGAAATCT 541
QY 293 ACGGCCCCCGCTCCGGCGGTGACTTGTGACAAACACCAAGCGCTTCGCGCTGTCTGCA 352
Db 542 ACGGGCCCGACGCGCGGACTACGAGACAAACAGCAGCGCTTCAGCTTCTCTGCC 601
QY 353 AGGCGCTATTTAGGCTGCCCGCTGCTGCCCTTC-----G 388
Db 602 AGGACGCTCGAGGACCCAGGATCTCAACCTCAACACAAACCCCTACTTTCTGGTC 661
QY 389 GCCCGCGGAGGACTCGCTTCTGTCGCAACGACTGGCAGCTCCGCGCTGGTCCCGTCC 448
Db 662 CTTACGGGAAGACGTGGTGTCTGTGCAACGACTGGACAGCGGCTTCTGGCCTGT 721
QY 449 TGTGTAAGACGAGTACCAAGCCCAAGGGCCAGTTCCAAAGGCCAAAGTCTGGCTA 508
Db 722 ACCTCAAGAGCAACTACCAAGTCCATGGCATCTACAGGAGGCCAAGGTGGCTTCTGCA 781
QY 509 TCCACAACATCGCTTCCAGGCGCGCATGTGGAGAGGCTTTCAAGGACACAAAGCTGC 568
Db 782 TCCACAACATCTCGTACAGGCGCGCTTCTCTTCGACGACTTTGCGCAGCTCAACCTGC 841
QY 569 CCGAGCGCGCTTTTGACAAAGTGGCTTCTCGAGCGCTATGCCAAGSTTTACACTGAGG 628
Db 842 CCGACAGTTCAGTCTGCTTCTGACTTCTATGACCGCTACGACAAG-----888
QY 629 CCACCCCATGGAGGAGGAGAGAGAGCCCGCTGCGGGAAGAGACCTACAAGAATCA 688
Db 889 -----CCCGTGGAGGGGCGC-----AAGATCA 910
QY 689 ACTGGCTGAAGGTCGATTTATGCGCGCGCAGCAAGCTGGTGTGCTGTGCCCAACTAGC 748
Db 911 ACTGATGAAGGCGGCGGATCTCTGAGGCGGACAAAGTGTGAGGTGAGCGCTACTACG 970
QY 749 CGACCGAGATCGCTCGGATCGCGCGGGGTGTGAGCTGGACACCGTCAATCCGCGCA 808
Db 971 CTGAGGAGCTATCTCTGGCAAGCCAGGGGTGCGAGTTCGACAAACATCATCGCGCTCA 1030
QY 809 AGGGCATTTGAGGCGCATTTGTAAGCGCATGACATTTGAGGAGTGAACCCCAAGACGCA 868
Db 1031 CGGGGATCACCGGAATCTGCAAGCGCATGCTGAGTGTGAGGACCCCAAGACGCA 1090
QY 869 AGTTCTGTCTGCGCGCTACGACCAAGAGTCTACGCGGCGCAAGCGCGCGCGCAAG 928
Db 1091 AGTTCTGCGCGCTCACTACGACATCACCGCGCTTGGAGCGCAAGCGCGCTGAACAAG 1150
QY 929 AGGCGCTGAGGCGCGGCTGCGCTGCTGTGACCCCGCGCGCGCTTTCGCGCTTCA 988
Db 1151 AGGCACTGAGGCGCGGCTGCGGCTGCGCGTGTGAGTGTGCGCTTGTGGCTTCA 1210
QY 989 TGGCGCGCTGAGGAGCAGAAAGGTTGTGGACATCATCTTGGCGCGCTTCCCAAGATCC 1048
Db 1211 TGGCGAGGCTGAGGAGCAGAAAGGCGCGCGTGTGATGATGCTATCCCGGAGATCC 1270
QY 1049 TGGCCACCCCAAGTGTGAGATCGCATCTCTGGTGTACGCGCAAGCGCGCTACGAGAGC 1108
Db 1271 TGAAGGAGGAGGACGCTCCAGATCATCTCTTGGCACCGGGAAGAGTTTGAAGC 1330
QY 1109 TGGTGAACGCGCATCGGCAAGTACAAGGCGCGCGCAAGGCGGTGTCAGATTTCTCG 1168
Db 1331 TGCTCAAGAGCAAGGAGAGAGTTCCCGGCAAGGTGAGGCGCGGTGTCAGTTCAAGC 1390
QY 1169 GCGCGCTGCGCACATGCTTCAACCGCGCGGCGGCTTCTGCTGTGGTGTGCGCTTCTCG 1228
Db 1391 GCGCGCTAGCTCACCAGATGATGGCGCGCGGCGGCTTCTGCTGTGCTGCTGCTGCTG 1450
QY 1229 AGCCCTGGGCGCTGATTCAGCTGACGCGATGCTACGCTACGCTGACGCTGCGGTAGCT 1288
```

Db	1451	AGCCGTGCGGCGCTATTCAGACTCCAGGAATGCCTATGGAAACCCGCTGCGGTGTGCGCGT	1510
QY	1289	CCACGGCGGCGCTGTGCACACCGCTCAAGSAGGCGCTACCGGTTCCACATGGGCGCC	1348
Db	1511	CCACGGCGGCGCTGCTGCACACGATCTGGGAGGCAACCTGTTTCCATATGGGCGGC	1570
QY	1349	TGA-----ACCOCACAGCTGGAGAGGCTGACGCCGACGCCCTTGGCGCCACACGTGC	1402
Db	1571	TCAGCTCGACTGCAACGTGTGGACCGCGCGACGTGAAGAGGTGGCGACCAACCTGTA	1630
QY	1403	GCGTGCCACGAGAGTGTTTGCGGCGGCCCTACCCCGAGATGTTGGCCCACTGCATCA	1462
Db	1631	AGCGGCGCTCAAGTCTGCGGCACGCCGCGCTACCAAGAGATGTTCAAGAACTGCATGA	1690
QY	1463	GCCAGACCTGTCTGTGCTCAAGCCCGCCCAAGAGTGGGAGGCGCTGCTGGAGAGGTGG	1522
Db	1691	TCCAGATCTCTCTTGAAGGAGACCTGCCAAGAACTGGAGAGCTGCTTCTGAACTGG	1750
QY	1523	TGTACGCCAAGGGCGCGTGGCCACCCGCCAAGAGAG	1560
Db	1751	GGGTGAGGGGACGACGCGGGGATCTGTCGGCGAGAG	1788

Search completed: June 3, 2003, 13:34:51
Job time : 2792.82 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 05:08:24 ; Search time 231.514 Seconds
(without alignments)
15495.523 Million cell updates/sec

Title: US-09-980-771A-8

Perfect score: 1593

Sequence: 1 gcgtgacatcgatggt.....ccgttgccgagaagatcccc 1593

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

```

1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	474.8	29.8	2267	18	AA63355
2	470	29.5	1915	19	AA63355
3	447.4	28.1	2542	19	AAV29753
4	344	21.6	1696	22	AAC86955
5	316.8	19.9	2161	24	ABK53210
6	298	18.7	2115	21	AAC32824
7	258	16.2	2183	24	ABK53215
8	221	13.9	2807	21	AAC86435
9	221	13.9	2842	21	AAC86411

10	218.2	13.7	2826	19	AAV01528	Wheat granule-boun
11	216.8	13.6	2097	19	AAV29755	zea mays soluble s
12	214.8	13.5	2423	19	AAV70958	DNA encoding maize
13	214	13.4	2107	21	AAC86412	Wheat starch synth
14	214	13.4	2107	21	AAC86434	Wheat starch synth
15	212.4	13.3	9024	21	AAC86431	Wheat SSII gene SE
16	210.2	13.2	2380	19	AAV66834	zea mays soluble s
17	210.2	13.2	2920	24	ABK88112	CDNA encoding modi
18	209.2	13.1	2478	18	AAT67287	Soluble starch syn
19	209.2	13.1	2939	21	AAC86410	Wheat starch synth
20	209.2	13.1	2939	21	AAC86433	Wheat starch synth
21	208.6	13.1	2946	24	ABK88115	CDNA encoding barl
22	208.6	13.1	2951	24	ABK88114	CDNA encoding barl
23	208.2	13.1	2950	24	ABK88113	CDNA encoding barl
24	207	13.0	2248	21	AAZ50651	Corn starch synth
25	206.6	13.0	1798	21	AAZ50651	Corn starch synth
26	206.6	13.0	2019	21	AAZ50646	Corn starch synth
27	203.8	12.8	1724	24	ABA01821	Rice starch synth
28	161	10.1	2007	19	AAV70959	DNA encoding maize
29	161	10.1	2007	19	AAV29754	zea mays soluble s
30	161	10.1	2085	18	AAT67286	Soluble starch syn
31	161	10.1	2085	19	AAV66833	zea mays soluble s
32	151	9.5	1479	24	ABO90258	M. capsulatus gene
33	151	9.5	1479	24	ABQ90406	M. capsulatus gene
34	125.6	7.9	333	21	AAC74569	Human ORFX ORF124
35	125.6	7.9	333	24	ABN18316	Human ORFX polynuc
36	118.2	7.4	2239	19	AAV01527	Wheat soluble star
37	118.2	7.4	2805	21	AAZ24487	Wheat soluble star
38	116	7.3	2662	20	AAK34651	CDNA sequence of w
39	110.6	6.9	2533	15	AAQ45183	Soluble rice starc
40	108	6.8	1758	17	AAQ32325	Soluble starch syn
41	106.4	6.7	1984	21	AAC46797	Arabidopsis thalia
42	102.6	6.4	1528	21	AAZ50637	Corn soluble starc
43	102.6	6.4	1620	19	AAV29759	zea mays pEX52 st
44	102.6	6.4	1749	19	AAV70960	DNA encoding maize
45	102.6	6.4	1752	19	AAV29756	zea mays soluble s

ALIGNMENTS

RESULT 1
AA63355
ID AAX63355 standard; cDNA; 2267 bp.
AC AAX63355;
XX
XX
16-JUL-1999 (first entry)
XX
DE Granule bound starch synthase encoding cDNA.
XX
KW Maize; corn; zea mays; delta-9 desaturase; GBSS; target; substrate;
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
XX
OS zea mays.
XX
PN WO9710328-A2.
XX
PD 20-MAR-1997.
XX
PF 12-JUL-1996; 96WO-US11689.
XX
PR 13-JUL-1995; 95US-0001135.
XX
PA (DOWC) DOWELANCO.
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Edington BE, Folkerts O, Guo L, McSwiggen JA, Merlo DJ;
PI Merlo PAO, Skokut TA, Young SA, Zwick MG;

DR WPI; 1997-202224/18.

XX Ribozyme which modulates plant gene expression - preferably

PT modulates expression of DELTA-9 desaturase or granule bound starch

PT synthase in maize or canola

XX Example 9; Page 31-33; 155pp; English.

FS The present invention describes an enzymatic nucleic acid molecule (I)

XX with RNA cleaving activity, which modulates the expression of a plant

CC gene. Also described is a gene comprising a cDNA sequence encoding maize

CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,

CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)

CC gene, in a plant (preferably a maize or canola plant). (I) can be used

CC to modulate caffeine synthesis in a coffee plant, nicotine production in

CC a tobacco plant, fruit ripening processes in an apple, tomato, pear,

CC plum or peach plant, flower pigmentation in a rose, petunia,

CC chrysanthemum or marigold plant or lignin production in a tobacco,

CC aspen, poplar or pine plant.

XX

SQ Sequence 2267 BP; 465 A; 699 C; 733 G; 370 T; 0 other;

Best Match 29.8%; Score 474.8; DB 18; Length 2267;

Best Local Similarity 59.9%; Pred. No. 6.2e-66;

Matches 978; Conservative 0; Mismatches 557; Indels 99; Gaps 7;

QY 5 TGGACATCGTGAATGTTGCTGAGTGGCGCCCTTGTGCTCCAAAGAGCGGCGCCCTGGGCG 64

DB 418 TGAAGCTGCTTCGTGCGCGCGAGATGGCGCCGTGGAGCAAGACCGCGCCCTCGGGG 477

QY 65 ATGTCACTGGTGGCTGCTATTGAGTGGTCAAGCGGGCCACCGCTCATGACCATG 124

DB 478 AGTCTCTGGCGGCTGCGCGCCCATGGCGGAAATGGGACCGCTGTCTATGTTGCTGCT 537

QY 125 CCCCCTCGTACACAGTACGTGACGCTGGGACACCTCGTGTGCTGGACAT----- 179

DB 538 CTCGCCGTACACAGTACAGGACGCTGGGACACACCGCTGCTGTCGAGATCAAGA 597

QY 180 -----CATGGCGGAGAGTCCGCTACTTCCACTCCATCAAGAGGCGCTGCACCGG 232

DB 598 TGGGAGACAGGTACGAGACGCTCAGTGTCTTCCACTGTACAAAGCGCGAGTGGACCGG 657

QY 233 TGTGATTAACACCCCTGTTCTTGGCCAAAGTCTGGGCAAGACCGCTCCAGCTGT 292

DB 658 TGTTCGTTGAACACCACTGTTCTTGGAGAGGTTTGGGAAAGACCGAGGAAGATCT 717

QY 293 ACGGCCCCGCTCGCGCGCTGACTACCTGGCAACACCAAGCGCTTGGCCCTGTTCTGCA 352

DB 718 ACGGCGCTGACCTGGACGAGTACAGGACACACCGCTGCGGTTTACGCTGTATGCC 777

QY 353 ACGGCGCTATTAGGCTGCCCGCGTGTGCTGCCCTTCGGC----- 390

DB 778 AGGCAGCACTTGAAGTCCAAAGGATCTCTGAGCTCAACAAACCAACATCTCTCCGGAC 837

QY 391 ---CCGCGGAGACTGCGTCTCTGTCGCAAGACTGSCACTCGCCCTGTTGCCGTTCC 448

DB 838 CATACGGGAGAGACTGCTGTCTGCTGCAAGACTGSCACACCGCCCTCTCTGCTGT 897

QY 449 TGCTAAGGACAGTACAGCCCAAGGCGCAGTTCCACAAAGGCCAAGTCCGTTGGCTA 508

DB 898 ACCITCAAGAGCACTACAGTCCACGGATCTACAGGACCAAGACCGCTTCTTCTGCA 957

QY 509 TCCACAACATCCCTTCCAGGCGCGCATGTGGGAGGAGGCTTTCAGGACACGAAGCTGC 568

DB 958 TCCACAACATCTCTTACCAGGCGCGGTTTCGCTTCTCGGCTTCTCGGCTTACCGGAGCTGACCTCC 1017

QY 569 CCCAGGCGCCCTTTCAGAGCTGGCGCTCTCGGACGGCTATGCCAAGGTTTACACTGAGG 628

DB 1018 CGGAGAGATTCAGTGTCTTCTGATTTTCATCGACGGCTTACGAGAAG----- 1064

QY 629 CCACCCCTATGAGGAGGACGAGAGAGCCCGCTGACGGGAAAGACCTACAAGAAGATCA 688

DB 1065 -----CCCGTGGAG-----GCCGGAAGATCA 1086

QY 689 ACTGCTGAAGGTGGCATTATCGCCGCGACAAAGCTGGTGTGCTGTGCGCCCACTACG 748

DB 1087 ACTGGATGAAGCCGCGGATCCTCGAGGCGGACAGGCTCTCACCCTGTCAGCCCTACTACG 1146

QY 749 CGACCGAGATCGTCCGATGCGCGCGCGGTGTGAGCTGAGACCCGCTCATCCGCGCCA 808

DB 1147 CCGAGAGCTCATCTCCGGCATCGCCAGGGGTGCGGAGTTCGACAAACATCTGCGCTCA 1206

QY 809 AGGGCATTCAGGGCATTTGAACGGCATGACATTCAGGAGTGAACCCCAAGACCGACA 868

DB 1207 CCGCATCACCGCATCTCAACGGCTGAGCTGACGAGTGGACCCCGACGAGGACA 1266

QY 869 AGTTCCTGTCTGCGCCCTACGACCAAGACAGCTCTTACCGCGCAAGGCGCGCGCAAGG 928

DB 1267 AGTACATCCCTGAAGTACGACGCTGTCGACGGCGCTGAGGCGCAAGGCGCTGAACAAG 1326

QY 929 AGGCCCTGACGCGCGAGCTGGGCTGCTGTGAGACCCACCGCCCTGTTGCGCTTCA 988

DB 1327 AGGCGCTGAGCGGAGTCCGGCTCCCGGTGAGACCGGAACATCCCGCTGGTGGCGTTCA 1386

QY 989 TCGGCGCCTGGAGGACAGAGGGTGTGACATCATCTTGGCGCGCCCTGCCCAAGATCC 1048

DB 1387 TCGGAGGCTGAGAGAGAGAGGACCGACGCTCATGGGCGCGCCATCCCGACCTCA 1446

QY 1049 TGGCCACCCCAAG-----GTGACATCGCATCTCTGCTGAGTACCGGCAAGGCGCGCTACGAGA 1105

DB 1447 TGGAGATGTTGAGGAGCTGCAGATCTGCTGCTGGCACCGGCAAGAAAGTTTCGAGC 1506

QY 1106 AGCTGTGAACCCATCGCACCAAGTACAGGCGCGCCGCGCAAGGCGCTGCTCAAGTCT 1165

DB 1507 GATGTCTATGAGCGCGGAGAGAGTTCCAGGCAAGTGGCGCGCTGGTCAAGTTCA 1566

QY 1166 CGGCGCCCTGGCGCACATCTCACCGCGCGCGCGCTTTCATGCTGGTGGCTCGCGCT 1225

DB 1567 ACGGCGCTGGCGCACCATCATGCGCGCGCGCGCTGCTGCGCTGTCACGACCGCT 1626

QY 1226 TCGAGCCCTGGCGCTGATCTCCAGCTGCACGCCATGCACTACGCTGCTGCGCTGGTAG 1285

DB 1627 TCGAGCCCTGGCGCTCATCCAGCTGCAGGGATGCGATACGGAACGCCCTGCGCTGCG 1686

QY 1286 CTTCCACCGCGCGCTGCTCGACCGTCAAGGAGGCGCTCACCGCTTCCACATGGCG 1345

DB 1687 CGTCCACCGCTGCTGCTCGACCGCTCATCGAAGGCAAGACCGGCTTCCACATGGCG 1746

QY 1346 CCGTGA-----ACCGCGACAGCTGGAGAGCTGACCGCGCGCGCTGGCGCGCACCG 1399

DB 1747 GCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1806

QY 1400 TGGCGCTGCCAGGAGTGTGTTGGGCGCGCGCTACCGCGAGATGTTGGCGCACTGCA 1459

DB 1807 TCGAGCGCGCTCAAGTGTGCTGCGCACCGCGCTACGAGGAGTGTGAGGAAGTCA 1866

QY 1460 TCGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1519

DB 1867 TGTTCAGGATCTCTCTGAGGCGCTGCGCAAGACCTGAGGAGACGCTGCTGCTGCTGCT 1926

QY 1520 TGTGTGAGGCGCGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1579

DB 1927 TCGGGTCCCG---GCGCGGAGCGAGGCTGCGAAGGCGGAGATCGCGCGCTGCGCA 1983

QY 1580 CCGAGAGATCCCG 1593

DB 1984 AGGAGAACGTGGCC 1997

RESULT 2

AAK60319

ID AAK60319 standard; DNA; 1915 BP.

XX

AC AAK60319;

XX

DT 23-AUG-1999 (first entry)

XX DNA sequence of the maize waxy gene.
 DE Non-glycogen-like polysaccharide production; fermentation; waxy gene;
 KW starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;
 KW non-starch branching gene; amylopectin; amylose; plant-like starch; ss.
 XX Zea mays.
 XX WO9844780-A1.
 XX 15-OCT-1998.
 XX 03-APR-1998; 98WO-US06660.
 XX 04-APR-1997; 97US-0042939.
 XX (EXSE-) EXSEED GENETICS LLC.
 XX Guan H, Keeling PL;
 XX WPI: 1998-568285/48.
 XX P-PSDB: AAY16604.
 XX Producing non-glycogen-like polysaccharides in bacteria, fungi or
 PT plants - transformed with genes for enzymes involved in starch or
 PT glycogen synthesis allows fermentative production of starches with
 PT engineered properties
 XX Disclosure: Fig 49; 150pp; English.
 XX The specification describes a method for the production of
 CC non-glycogen-like polysaccharides in a host. The method comprises
 CC transforming a host, suitable for fermentation, with genes encoding
 CC starch- or glycogen-synthesis enzymes, and fermenting the transformants.
 CC The specification also describes hosts transformed with a gene active
 CC in glycogen synthesis and at least one non-starch branching gene.
 CC involved in production of amylopectin or amylose in its original host.
 CC The method is used to produce plant-like starches by fermentation and
 CC new starches in plants. These starches are useful for all food and
 CC non-food applications of starch. The present sequence is used in
 CC the course of the invention.
 XX Sequence 1915 BP; 365 A; 610 C; 641 G; 299 T; 0 other;
 SQ

Query Match 29.5%; Score 470; DB 19; Length 1915;
 Best Local Similarity 59.7%; Pred. No. 3.5e-65;
 Matches 975; Conservative 0; Mismatches 560; Indels 99; Gaps 7;

QY 5 TGGACATCGTGATGTTGCTGAGTGGCGCCCTTGGTCCCAAGAGCGGCGCCTGGGG 64
 DB 230 TGAAGTCGTCTTCGTCGCGCGGAGATGGCGCGGTGGAGCAAGACCGCGGCTCGGG 289

QY 65 AITGACTGGTGGCTGCTATTGACTGGTGAAGCGCGGCCACCGCGTCATGACCATG 124
 DB 290 ACGTCTCGGCGGCTGCGCGCGGCATGGCGCGAAGCGGACCGTGTGCTGCT 349

QY 125 CCCCTCGCTACACCACTACGCTGAGCGCTGGGACACCTCGGTGGTGGGACATCA 181
 DB 350 CTCGCCGTACACCACTACAGGAGCGCTGGGACACCACTCGGTGGTGGGACATCA 409

QY 182 -----TGGCGGAGAGGTTCGCTACTTCCACTCCATCAAGAGGCGGTGCACCGG 232
 DB 410 TGGGACAGGGTACAGACGGTTCAGTTCTCCACTGTACAGCGCGGAGTGGACCGG 469

QY 233 TGTGATTGACACCCCTGGTTCCTGGCAAGGTCTGGGGCAAGACCGGCTCCAACTGT 292
 DB 470 TGTTCGTGACCACTGTTCTTGGAGAGGTTTGGGGAAGAGGAGGAGAGATCT 529

QY 293 ACGGCGCGGCTCGGCGGTGACTACCTGGACCAACCAAGCGCTTCGCCCTGTGTGCA 352
 DB 530 ACGGCGCTGTGCTGGAACGGACTACAGGACCAAGCAGCTGCGGTTGAGCTGTATGCC 589

QY 353 AGGCGCTATTGAGGCTGCCGGTGGCTGCTGCCCTTCGGC----- 390
 DB 590 AGGAGCACCTTGAAGCTCCAAAGGATCCTGAGCCTCAACAACACCCATACTTCTCCGAC 649

QY 391 --CCGCGGAGGAGTGGTCTTGTGGCCCAACGACTGGCACTGGCCCTGGTGGCCGCTCC 448
 DB 650 CATACGGGAGGAGCTGCTGTTGCTGTGCAACGACTGGCACTGGCCCTGCTCTCGTCT 709

QY 449 TGCTGAAGGACGAGTACACGCCCAAGGCCAGTTTCAACCAAGGCCAAGTGGTGGCTA 508
 DB 710 ACCTCAAGACCACTACCACTCCACGGCATCTACAGGAGCAAGACGCTTCTTGTGCA 769

QY 509 TCCACAACATCGCTTCCAGGGCGCATGTGGAGGAGGCTTTCAAGGACACCAAGCTGC 568
 DB 770 TCCACAACATCTCTACAGGCGCGTTCGCTTCTCCGACTACCGGAGCTGAACCTCC 829

QY 569 CCCAGGCGCGCTTTGACAAGCTGGCCTTCTCGACGCGCTATGCCAAGTTTACATGAGG 628
 DB 830 CGGAGAGATCAAGTCGCTCTTCGATTTCATGACGCGCTACGAGAAG----- 876

QY 629 CCACCCCATGGAGGAGGACGAGAAGCCCGCTGACGGGAAAGACCTCAAGAAGATCA 688
 DB 877 -----CCGCTGGAAG-----GCCGGAAGATCA 898

QY 689 ACTGGCTGAAGGTGGCATTAATCCGCGCCGACAAAGCTGTGCTGTCGCCCAACTACG 748
 DB 899 ACTGGATGAAGGCGGGATCCTCGAGGCCACAGGGTCTTCACCGTCAGCCCTACTACG 958

QY 749 CGACCCGAGATCGCTGCGGATGCGCGCGGCTGTGGAGCTGGACACCGTTCATCGCGCCA 808
 DB 959 CCAGGAGCTCAATCTCCGGCATCGCAGGGGCTGCGAGCTCGACACATCATCGGCTCA 1018

QY 809 AGGSCATTGAGGCGATTGTAACGGCATGGACATTCAGGAGTGGAAACCCCAAGACGACA 868
 DB 1019 CCGGCATCAACCGCATCGTCAACGGCATGACGTACGAGTGGAGCCCAAGAGGACA 1078

QY 869 AGTTCCTGTGCGCCCTTAGGACCAAGACGTCTACGCCGCGCAAGCGCGCGCAAGG 928
 DB 1079 AGTACATCCGCTGAAGTACGACGTGTGACGCGCTGGAGGCCAAGGGGCTGAACAAG 1138

QY 929 AGSCCTTGACGCGGAGCTGGGCTGCTGCTGGACCCCAAGCGCCCTGTTCCGCTTCA 988
 DB 1139 AGCGCTGACGCGGAGTGGGCTCCGCTGACCGGAACATTCCTGCTGGCTGGCTTCA 1198

QY 989 TGGCGCGCTGGAGGACAGAGGCTGTGACATCATCTTGGCGCGCTGCCCAAGATCC 1048
 DB 1199 TCGGAGGCTGGAAGAGCAGAGGCGCCGACGTCTATGCGCGCGCCATCCCGCAGCTCA 1258

QY 1049 TGGCCACCCCAAG-----GTGACATGCCATCTCTGGGTACCGGCAAGCGCGCTACGAGA 1105
 DB 1259 TGGAGATGTTGAGGAGCGTGCAGATCTTCTGCTGGGCACGGGCAAGAGATTGAGC 1318

QY 1106 AGTGTGTGAACGCCATCGGCACCAAGTACAAGGCGCGCGCAAGGCGGTGGTCAAGTCT 1165
 DB 1319 GCATGCTCATGAGCGCGGAGGAGAGTTCCAGGCAAGGTGCGCGCTGGTCAAGTTCA 1378

QY 1166 CGGCGCGCTGGCGCACATGCTCACCGCGCGCGCGACATTCATGCTGGTGGCTCGCGCT 1225
 DB 1379 ACGCGCGCTGGCGCACCATCATGCGCGCGCGCGACGTGCTGCGCGTCCACGCGCT 1438

QY 1226 TCGAGCGCTGGCGCTGATCCAGCTGCAGCCATGACGTACGTACGTGCGCGCTGGTAG 1285
 DB 1439 TCGAGCGCTGGCGCTCATCCAGCTGCGAGGGATGATACGAGCGCTGCGCGCTGGC 1498

QY 1286 CTTCACCGCGCGCTGGTTCGACACCGTCAAGGAGGCGCTCACCGCTTCCACATGGCG 1345
 DB 1499 CGTCCACCGGTGAGCTGCTGACACCATCATCGAAGGCAAGACCGGCTTCCATGGGCG 1558

QY 1346 CCTGAACCCCG-----ACAAGCTGGAGAGGCTGACCGCGCGCTGGCGCGCACCG 1399
 DB 1559 GCTCAGGCTGACATGTAACGTCGTGAGCGCGGCGACCTCAAGAGGTTGGCCACCAT 1618

QY 1400 TCGCGCGTCCAGCGAGGTGTTTGGGGCGCGGCTTACCCCGAGATGTTGGGCAACTGCA 1459

```

1619 TCCAGCGCCATCAAGTGTGTCGACGCCGCGCTACGAGGAGATGTTGAGAACTGCA 1678
1460 TCAGCCAGGACTGCTGTTCCAGAGCGCCGACAGAGTGGAGGCGCTGCTGGAGAGG 1519
1679 TGATCCAGGATCTCTCCGAGAGGCGCTGCCAAGAACTGGAGAACGCTGCTCAGCC 1738
1520 TGGTGTAGCGCAAGGCGCGTGGCCACCGCCCAAGAGGAGAGATCAAGGTGCGCGTGG 1579
1739 TCGGGGTGCC---GGCGGAGCAGGAGTGAAGGCGAGGATCGCGCGCTCGCA 1795
1580 CCGAAGATCCCC 1593
1796 AGGAGAAGCTGGCC 1809

```

RESULT 3

AAV29753
ID AAV29753 standard; DNA; 2542 BP.

AC AAV29753;

DI 11-SEP-1998 (first entry)

DE Oryza sativa waxy gene.

KW SER; starch-encapsulating region; fusion vector;

KW starch synthase; bacterial glycoen; ss.

OS Oryza sativa.

XX Key Location/Qualifiers

PH 453..2282

FT /*tag= a

FT /product= starch (bacterial glycoen) synthase

FT polyA_site

FT 2535

FT /*tag= b

PN WO9814601-Al.

XX 09-APR-1998.

XX 30-SEP-1997; 97WO-US17555.

XX 30-SEP-1996; 96US-0026855.

XX (EXSE-) EXSEED GENETICS LLC.

XX Guan H, Keeling P;

XX WPI; 1998-240100/21.

XX P-PSDB; AAW56485.

XX Hybrid polypeptide comprising starch-encapsulating region and

XX protein - useful for, e.g. producing protein(s) resistant to

XX degradation by stomach acids

XX Example 2; Page 32-34; 156pp; English.

XX The sequence is that of the waxy gene which codes for starch

XX synthase. It can be used in the production of a hybrid

XX polypeptide comprising a starch-encapsulating region (SER) fused

XX to a payload protein. The hybrid polypeptide can be used to make

XX modified starches comprising the payload protein, selected from,

XX e.g. hormones, growth factors, antibodies, enzymes, dyes,

XX immunoglobulins, etc. The modified starch can also be used

XX to provide grain feeds enriched in amino acids. By encapsulating

XX the payload protein in starch, it is more resistant to

XX degradation by stomach acids.

XX Sequence 2542 BP; 610 A; 665 C; 693 G; 574 T; 0 other;

XX Query Match 28.1%; Score 447.4; DB 19; Length 2542;

```

Best Local Similarity 58.6%; Pred. No. 1.2e-61;
Matches 930; Conservative 0; Mismatches 561; Indels 96; Gaps 5;

QY 5 TGGACATCTGATGTTGCTGCTGAGTCCGCCCTTGGTCCAGAGCGCGGCTGGGCG 64
DB 700 TGAACGTCTGTTGCTGCGCGCGAGATGCCCTTGGAGCAGAGCCGCGGCTGGTG 759
QY 65 ATGTGACTGTGGCTGCTGCTATTTGAGCTGGTCAAGCGCGCCACCGCTCATGACCATG 124
DB 760 AGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819
QY 125 CCGCTCGTACGACAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 184
DB 820 CTCTCTGCTACGACAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 879
QY 185 -----CGAGAAGGTCGCTACTTCCACTCCATCAAGAAGGCGGTGACCGCG 232
DB 880 TTGCACAGAGTACGAGAGGCTGAGGTTTTCATTTGCTACAGCGTGAGTGCACCGTG 939
QY 233 TGTGATTGACCAACCGCTGCTTCTGCGCAAGCTCTGGGSCAAGACCGGCTCCAGCTGT 292
DB 940 TGTTCATCGACCATCGTCTATCTCTGAGAAGGTTTGGGAAAGACCGGTGAGAAGTCT 999
QY 293 AGGGCCCCGCTCCGCGCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352
DB 1000 ACGGACCTGACACTGGAGTTGATTACAAAGACCAACAGATGCGTTTTCAGCCTTCTTTGCC 1059
QY 353 AGGCGCTATTGAGGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 393
DB 1060 AGGACACTGAGGCTCTAGATCTTAACCTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1119
QY 394 -----GGGAGGACTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 448
DB 1120 CTTATGCTGAGGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1179
QY 449 TCGTGAAGCAGTACGACCGCCAGGCGCAGTTTCAACAGGCGCAAGTCTGCTGCTGCTGCTGCT 508
DB 1180 ACCTGAAGAACAACTACCGCCCAATGGCATCTACAGAAATGCAAGGTTGCTTCTGCTGCTGCT 1239
QY 509 TCCACAACATCGCTTCCAGGCGCGATGTTGGAGAGAGGCTTCAAGGACACAGGCTGCTGCTGCT 568
DB 1240 TCCACAACATCTCTACCGAGGCGGCTTTCGCTTTTCGAGGATTACCTGAGCTGAAGCTCT 1299
QY 569 CCGAGCGCGCTTTGACAGCTGCTGCTTCTGCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 628
DB 1300 CCGAGAGGTTGAGGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1343
QY 629 CCACCCCGCTGAGGAGGACGAGAGCCCGCTGAGGAGAGAGCTTCAAGAGATCA 688
DB 1344 -----ACGCCGTGGAGGCGAGGATCA 1368
QY 689 ACTGGCTGAAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 748
DB 1369 ACTGGATGAAGCGCGAATCTCTGGAAGCCGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
QY 749 CGACCCAGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 808
DB 1429 CCGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1488
QY 809 AGGCGATTGAGGCGCTTGTGACGCGATGACATTTGAGGAGTGAACCCCAAGACCGAC 868
DB 1489 CCGGATCACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548
QY 869 AGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
DB 1549 AGTACATACCGCGCAAGTACGACCGCAACCGGCAATTCGAGGCGAGGCGGCTGCAACAGG 1608
QY 929 AGGCGCTGACGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 988
DB 1609 AGGCGTTGACGCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1668
QY 989 TCGGCGCGCTGAGGAGCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1048

```

```

Db 1669 TCGGAGGCTGGAGAACAGAGGCGCTGACGTATGCGCGCGGCATCCCGGAGCTCA 1728
QY 1049 TGGCCACCCCAAGGTGCAGATCGCCATCTGGGTACCGCAAGCGCGCTACGAGAAGC 1108
Db 1729 TG---CAGGAGGACGTCAGATCGTTCTTCTGGGTACTGGAAGAAAGAACTCGAGAAGC 1785
QY 1109 TGGTGAAGCCATCGGACCAACATACAAAGGCGCGCCCAAGGGCGGTGCTCAAGTTCGCG 1168
Db 1786 TGTCAAGACATGAGGAGAGATATCCGGGCAAGGTGAGGGGGGTGGTGAAGTTCAACG 1845
QY 1169 CGCCCTTGGCGCATCTCATCCGCGCGCGCCGACCTTCATGCTGGTGCCCTCGCGCTTCG 1228
Db 1846 CGCGCTTGTCTATCATCATGATGCGCGGACCGACGTGCTCGCGTCCCGACGCGCTTCG 1905
QY 1229 AGCCCTGCGGCTTATTCAGTCTGACGCCATGACCTACGCTACCGTACCGTGGTACGCT 1288
Db 1906 AGCCCTGTGACATCATCACTGACGGGATGAGATACGGAAGCGCCCTGTGCTTGCCTG 1965
QY 1289 CCACGCGCGCTGTGTCGACACCTCAAGAGGCGCTCACCGGCTTCCACATGGCGCCC 1348
Db 1966 CCACGCGTGGCTGCTGGACACCGTATCAAGAGGCAAGACTGGTTTCCACATGGCGGTC 2025
QY 1349 TGAACCCCGAC-----AAGCTGAGCAGGCTGACGCGCGCGCTGGCGCGCCACCGTGC 1402
Db 2026 TCAGCGTCGACTCAAGGTGGTGAGCCAAAGCGAGCTGAAGAGGTGGCGGCCACCTGA 2085
QY 1403 GCGGTCCAGCAGAGTGTGTTGCGGGCGCGCTACCCCGAGATGGTGGCCAACTGCATCA 1462
Db 2086 AGCGCCCATCAAGGTGCTGCGGACGCGCGCTACGAGGAGATGGTCAAGAACTGCAIGA 2145
QY 1463 GCAGGACCTGTCTGTGTCAAGCGCGCCAGAAAGTGGGAGGCGCTGCTGGAGGAGGTGG 1522
Db 2146 ACCAGGACCTCTCTGGAAGGCGCTTCGGAAGAACTGGGAGAAATGTCTCTGGCGCTGG 2205
QY 1523 TGTACGGCAAGGCGCGGTGGCCACCG 1549
Db 2206 GCGTCGCGGACGCGCGGGGATCG 2232

RESULT 4
AAC86955
ID AAC86955 standard; cDNA; 1696 BP.
AC
AC AAC86955;
DT
DT 02-APR-2001 (first entry)
DE
DE cDNA encoding a granule bound starch synthetase II (GBSSII).
KW Granule bound starch synthetase II; GBSSII; starch grain;
KW adenosine diphosphate glucose-alpha,4-glucan alpha4-glucosyltransferase;
KW starch synthetase; ds.
OS Chlamydomonas reinhardtii.
FH
FH Key
FT Location/Qualifiers
FT CDS
FT 3..719
FT /*tag= a
FT /*product= "granule bound starch synthetase II (GBSSII)"
PN FR2793806-A1.
XX
XX 24-NOV-2000.
XX
XX 21-MAY-1999; 99PR-0006494.
XX
XX 21-MAY-1999; 99PR-0006494.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Dhulst C, Ball S;
XX
XX WPI; 2001-052291/07.
XX

```

```

DR P-PSDB; AAB311175.
XX
PT New recombinant nucleic acid encoding fusion of starch synthase and
PT second component, useful in pharmaceutical and food compositions, is
PT targeted to starch granules.
XX
XX Claim 3; Fig 1; 52pp; French.
XX
CC The present sequence encodes a granule bound starch synthetase II
CC (GBSSII). The specification describes a recombinant nucleic acid,
CC comprising a polynucleotide encoding an adenosine diphosphate
CC glucose-alpha,4-glucan alpha4-glucosyltransferase or starch
CC synthetase, placed upstream of a sequence that encodes a polypeptide
CC of interest. The adenosine diphosphate glucose-alpha,4-glucan
CC alpha4-glucosyltransferase protein can migrate to sites of
CC biosynthesis of starch grains in plant cells, becoming associated
CC with these grains. The recombinant nucleic acid sequence is used to
CC target polypeptides of interest to starch grains.
XX
SQ Sequence 1696 BP; 347 A; 509 C; 571 G; 269 T; 0 other;
Query Match 21.6%; Score 344; DB 22; Length 1696;
Best Local Similarity 100.0%; Pred. No. 1.8e-45;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1250 TGCACGCCATGCACTACGGTACCGTACCGTGGCGGCTTCCACCGCGGCTGTGTCGACA 1309
Db 13 TGCACGCCATGCACTACGGTACCGTACCGTGGCGGCTTCCACCGCGGCTGTGTCGACA 72
QY 1310 CCGTCAAGGAGGGGTCACCGGCTTCCACATGGCGGCTTGAACCCCGACAAGTGGACG 1369
Db 73 CCGTCAAGGAGGGGTCACCGGCTTCCACATGGCGGCTTGAACCCCGACAAGTGGACG 132
QY 1370 AGGCTACGCGCGAGCGCTTCCCGCCACCGTGGCGGCTTCCAGGAGGTGTTTGGGGCG 1429
Db 133 AGGCTACGCGCGAGCGCTTCCCGCCACCGTGGCGGCTTCCAGGAGGTGTTTGGGGCG 192
QY 1430 GCGCTACCGCGAGATGGTGGCCAACTGCATCAGCCAGGACCTGTCTGTGTCGAAGCCCG 1489
Db 193 GCGCTACCGCGAGATGGTGGCCAACTGCATCAGCCAGGACCTGTCTGTGTCGAAGCCCG 252
QY 1490 CCCAGAGTGGAGGCGCTGCTGGAGGAGGTGGTGTACGGCAAGGGCGGCTGGCCACCG 1549
Db 253 CCCAGAGTGGAGGCGCTGCTGGAGGAGGTGGTGTACGGCAAGGGCGGCTGGCCACCG 312
QY 1550 CCAGAGAGGAGGAGATCAAGGTGCGCCCTTCCGAGAGATGCCCC 1593
Db 313 CCAGAGAGGAGGAGATCAAGGTGCGCCCTTCCGAGAGATGCCCC 356

RESULT 5
ABK53210
ID ABK53210 standard; DNA; 2161 BP.
XX
XX AC ABK53210;
XX
XX DT 14-AUG-2002 (first entry)
XX
XX DE Potato granule-bound starch synthase I (GBSSI) DNA sequence.
XX
XX KW Starch; amylose; cereal crop; commodity starch; thickened foodstuff;
XX KW bread; baking; pasta; potato; granule-bound starch synthase I; GBSSI; ds.
XX
XX OS Solanum tuberosum.
XX
XX PN WC200218606-A1.
XX
XX PD 07-MAR-2002.
XX
XX PF 28-AUG-2000; 2000WO-US23494.
XX
XX PR 28-AUG-2000; 2000WO-US23494.
XX

```

PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Broglie K, Lightner J;
XX
DR WPI; 2002-404556/43.
XX
PT Novel starch isolated from cereal crop with a modification of amylose
PT content and/or amylose weight distribution relative to commodity starch
PT from same species of the cereal crop, for preparing thickened
XX foodstuffs
PS
XX Example 1; Page 36; 44bp; English.
CC The present invention relates to a new starch comprising amylose,
CC where the starch is isolated from a cereal crop, and comprises a 50%
CC increase in average molecular weight relative to commodity starch from
CC the same species of the cereal crop from which starch was isolated.
CC The starch of the invention is useful for preparing thickened foodstuffs
CC by combining the starch, a foodstuff and water and cooking the resulting
CC composition as necessary to produce a thickened foodstuff. The invention
CC is also useful for preparing foodstuffs such as breads, baked goods,
CC pastas, etc. The present nucleic acid sequence represents the potato
CC granule-bound starch synthase I (GBSSI) DNA sequence that was used in
CC the methods of the invention for generation of a potato full-length
CC sense GBSSI DNA construct.
XX
SQ Sequence 2161 BP; 614 A; 428 C; 505 G; 614 T; 0 other;

Query Match 19.9%; Score 316.8; DB 24; Length 2161;
Best local Similarity 53.8%; Pred. No. 3.2e-41;
Matches 836; Conservative 0; Mismatches 622; Indels 96; Gaps 5;

QY 5 TGGACATCGTATGTTGCTGCTGAGTCCGCGCTTGTGCTCAAGACGGCGCTGGCG 64
DB 278 TGAACCTGATCTTTGGGGTACTGAGTGTGCTTGTGACCAAACTGGTGACTAGTG 337
QY 65 ATGTGACTGGTGGCTGCTATTTAGTGTGCTCAAGCGCGCCACCGCTCATGACCAATG 124
DB 338 ATGTTCTTGGTGGATACCAACGAGCTTGGACGCGCGGACATCGGTAAATGACAATAT 397
QY 125 CCCTCGCTACACAGTACGCTGAGCGCTGGGACACCTCGGTGCTGCGGACATCATG 184
DB 398 CCCCCGTTATGACCAATACAAAGATGCTTGGGATACTAGCGTTGCGGTTGAGGTCAAG 457
QY 185 -----GCGAAGAGTCCGCTACTTCCACTCCATCAAGAGGCGCTGCACCGG 232
DB 458 TTGGAGACAGCATGAAATTTGTTGCTTTCTTCACTGCTATAAAGCGTGGGTGATCGTG 517
QY 233 TGTGATTCACACCGCTGCTTCTGGCCAGGTCTGGGGCAAGACCGGCTCCAGCTGT 292
DB 518 TTTTGTGGACACCAATGTTCTTGGAGAAAGTTTGGGGCAAACTGGTTCAAAATCT 577
QY 293 ACGGCGCGCTCCGGCGCTGACTACTCGACAAACCAAGCGCTTCGCCCTTCTGCA 352
DB 578 ATGGCCCCAAGCTGGACTAGTATTATCTGGACAAATGAATAGTTAGTTCAGTTGTTGTC 637
QY 353 AGCGCGCTATTGAGCTGCGCGCTGCTGCCCTTCGCG----- 390
DB 638 AAGCAGCCCTAGAGGCACTAAAGTTTGAATTTGAACAGTAGCAACTACTTCTCAGGAC 697
QY 391 ---CCGGCGAGAGCTGCTTCTGTTGGCCCAAGCTGGCACTCCGCGCTGGTCCCGTCC 448
DB 698 CATATGGAGAGGATGTTCTTCTTCAATGCGCAATGATTGGCACACAGCTCATTTCTTGT 757
QY 449 TGTGAAGGAGGAGTACCAAGCCCAAGGCGGCTTCAACAGGCGAGTCCGCTGGCTA 508
DB 758 ACTTGAAGTCAATGTACCAAGTCCAGAGGAATCTATTGATGCCAAGTGCCTTCTGCA 817
QY 509 TCACAAACATTCGCTTCGAGGGCGCAATGTTGGAGAGGCTTTCAAGGACACGAACTGC 568
DB 818 TCATAACATTTGCTTCAAGGCGGATTTTCTTCTCTGACTTCCCTCTTCTCAATCTTC 877
QY 569 CCAGGCGCGCTTTGACAACTGCGCTTCTCGGACGCGCTATGCCAAGTTTACACTGAG 628

Db 878 CTGATGAATTCAGGGGTTCTTTGATTTCATTCGATGATGAGAAGCCCTGTTAAGG--- 934
QY 629 CCACCCCCATGGAGGAGGAGGAGAGCCGCCCTGACGGGAAGACCTACAGAAGATCA 688
Db 935 -----GTAGGAAATCA 946
QY 689 ACTGGCTGAAGGTGGCATATTATCGCGCCGACAAAGCTGGTACTGTGTCGCCCAATACG 748
Db 947 ACTGGATGAAGCTGGGATATTAGAAATCATAGAGGTGGTTACAGTGAGCCCATATATG 1006
QY 749 CGACCGAGATCGCTGCCGATGCGCGCGGTGTGAGGTGGACACCGTCATCCGCGCCA 808
Db 1007 CCCAAGAACTGTCTCTGCTGTGACAAGGGTGTTCAAATTTGGACAGTGTCTTCTGTAAGA 1066
QY 809 AGGGCATTCAGGCGCATTTGACGGCATGCACATTCAGGAGTGAACCCCAACAGCGACA 868
Db 1067 CTTGCACTACTGGATGTGAATGGCATGATACACAGAGTGGAAACCCAGCGCTGACA 1126
QY 869 AGTTCCTGTCTGCGCCCTACGACCAAGACAGCGCTCTACGCCGCAAGCGCGCCCAAGG 928
Db 1127 AATACACAGATGTCAAATACGATATACCACTGTCTATGGACGCAAAACCTTTACTAAGG 1186
QY 929 AGSCCTTCAGCGCGAGCTGGGCTGCTGTGACCCCGCCCGCCCTGTTCCGCTTCA 988
Db 1187 AGGCTCTTCAAGCAGCAGTTGGCTTGCCTGTTCACAAGAAAGATCCCTTTGATTGGCTTCA 1246
QY 989 TCGCGCGCTGGAGGAGCAGAGGGTGTGGACATCATCTTGGCGCGCTCCCAAGATCC 1048
Db 1247 TCGGACAGCTTGGAGAGCAGAGAGTTTCAGATATTCTTGTGTCGAATTCACAAGTTCA 1306
QY 1049 TGCCCAACCCCAAGTGTGACATCCCATCTGCTTACCGGCAAGCGCGCTACGAGAAGC 1108
Db 1307 T---CGGATTGGATTTCAAATTTGTTAGTCTCTTGAATGSCAAAAGAGGAGTTTGCAGG 1363
QY 1109 TGTGAAGCGCATTCGACCAAGTACAAAGGCGCGCCGCAAGGCGGTGCTCAAGTTCTCGG 1168
Db 1364 AGATTGAACAGCTTCGAAGTGTTCACCCCTAACAAAGCTAAAGAGTGGCAAAATTCAGT 1423
QY 1169 CGCCCTGGCGGCACTGCTCACCGCGCGCGCTCATGCTGCTGGTGGCGCTCGCGCTTCG 1228
Db 1424 TCCTTTGGCTCACATGATGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1483
QY 1229 AGCCCTGCGGCTGATCCAGCTGCAGCCCATGCACTACGCTACGCTGCGCGCTGGTAGCCT 1288
Db 1484 AACCTTGTGCTCAATTCAGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1543
QY 1289 CCACGCGCGCTTGTGCTGACACCGTCAAGGAGGCGCTCACCGCTTCCACATGGCGGCC 1348
Db 1544 CGACTGCTGACTGTGTGACACTGTGAAGAGGCTATATCTGATTCATATGAGGAGCCT 1603
QY 1349 TGA-----ACCCCGCAGCAAGCTGGAGGCTGACGCGCGAGCGCTGGCGCGCCACCGTGC 1402
Db 1604 TCAATGTTGAATCGATGTTGTTGACCCAGCTGATGCTGCTTAAGATAGTAAACAAGTTG 1663
QY 1403 GCGTGGCAGGAGTGTGTTGGGGGGCGGCTACCCCGAGATGGTGGCGCACTGATCA 1462
Db 1664 CTAGAGCTCTTGGAGTCTATGGCAACCTCGCATTTGCTGAGATGATAAAAAATTTGCTATG 1723
QY 1463 GCCAGGACCTTCTGCTGCTCAAGCGCGCCAGAGTGGGAGGCGCTGCTGCGAG 1516
Db 1724 CAGAGGAACCTCTCTGGAGGAACCTGCGCAAGAAATGGGAGACATTTGCTATTGG 1777

RESULT 6
AAC32824
ID AAC32824 standard; DNA; 2115 BP.
XX
AC AAC32824;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 779.

XX	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EPI033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126284.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.
PR	23-APR-1999; 99US-0130510.
PR	28-APR-1999; 99US-0130891.
PR	30-APR-1999; 99US-0131449.
PR	30-APR-1999; 99US-0132048.
PR	30-APR-1999; 99US-0132407.
PR	04-MAY-1999; 99US-0132484.
PR	05-MAY-1999; 99US-0132485.
PR	06-MAY-1999; 99US-0132486.
PR	06-MAY-1999; 99US-0132487.
PR	07-MAY-1999; 99US-0132883.
PR	11-MAY-1999; 99US-0134256.
PR	14-MAY-1999; 99US-0134218.
PR	14-MAY-1999; 99US-0134219.
PR	14-MAY-1999; 99US-0134221.
PR	14-MAY-1999; 99US-0134370.
PR	18-MAY-1999; 99US-0134768.
PR	19-MAY-1999; 99US-0134941.
PR	20-MAY-1999; 99US-0135124.
PR	21-MAY-1999; 99US-0135353.
PR	24-MAY-1999; 99US-0135629.
PR	25-MAY-1999; 99US-0136021.
PR	27-MAY-1999; 99US-0136392.
PR	28-MAY-1999; 99US-0136782.
PR	01-JUN-1999; 99US-0137222.
PR	03-JUN-1999; 99US-0137528.
PR	04-JUN-1999; 99US-0137502.
PR	07-JUN-1999; 99US-0137724.
PR	08-JUN-1999; 99US-0138094.
PR	10-JUN-1999; 99US-0138540.
PR	10-JUN-1999; 99US-0138847.
PR	14-JUN-1999; 99US-0139119.
PR	16-JUN-1999; 99US-0139452.
PR	16-JUN-1999; 99US-0139453.
PR	17-JUN-1999; 99US-0139492.
PR	18-JUN-1999; 99US-0139454.
PR	18-JUN-1999; 99US-0139455.
PR	18-JUN-1999; 99US-0139456.
PR	18-JUN-1999; 99US-0139457.
PR	18-JUN-1999; 99US-0139458.
PR	18-JUN-1999; 99US-0139459.
PR	18-JUN-1999; 99US-0139460.
PR	18-JUN-1999; 99US-0139461.
PR	18-JUN-1999; 99US-0139462.
PR	18-JUN-1999; 99US-0139463.
PR	18-JUN-1999; 99US-0139750.
PR	18-JUN-1999; 99US-0139763.
PR	18-JUN-1999; 99US-0139817.
PR	22-JUN-1999; 99US-0139899.

```
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 26-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 18.7%; Score 298; DB 21; Length 2115;
Best Local Similarity 53.7%; Pred. No. 2.8e-38;
Matches 820; Conservative 0; Mismatches 610; Indels 96; Gaps 6;

QY 20 TTGCTGCTGAGTGCCTCCCTGCTCCAGACGGCGGCTGGCGGATGACTGGTGGCC 79
DB 415 TTGGAGCTGAAGTTGGTCCATGAGATTAACCTGGTGGTCTTGGTGAATGTTCCGGTGGTTC 474
QY 80 TGCCTATTGAGTGGTCAAGCGCGCCACCGCTCATGACCATGTCCTCCCTGCTAGCACC 139
DB 475 TACCTCCAGCTTCTGCTGTAGAGCCACCGCTGTGATGACAAATTTGCTCCTCGTATGACC 534
QY 140 AGTAGCTGACGCTTGGACACCTCGGTGGTGTGCTGGACATC-----ATGGGG 187
DB 535 AATATAAAGATGCTTGGGACCATTTGTTGGTTCAGATCAAAAGTTGGGGATTAAGTTG 594
QY 188 AGAAGTCCGCTACTTCCACTCCATCAAGAAGGCGGTGCACCGGTGTGGATTGACAC 247
DB 595 AGAATGTTCTTCTTCCATTCCTACAAACAGAGGAGTGTGATCGTCTTGTGTTGACCATC 654
QY 248 CTTGTTCTTCTGCGCAAGTCTTGGGCAAGACCGGTCCCAAGCTGTACGCGCCCGCTCGC 307
DB 655 CAATCTTTCTTGTAAAGTTGTGGGCAAAACAGGATCCAAAATCTATGCTCTATAACTG 714
QY 308 GCGCTGACTTACCTGGACACACAGCGCTTCGCCCTGTCTTCACAGGCGCGCTATTGAGG 367
```

```
DB 715 GAGTAGACTACAAATGACACCAACTCCGGTTCAGTTTGTGTGAGGCTGCTCTTGAGG 774
QY 368 CTGCGCGGTGCTGCCCTTCGGCCCGGGGAGGACTGC-----405
DB 775 CACCACAGGTTCTGAACCTTGAACAGAGCAAGTACTCTCTCGACCATATGTTGAAGATG 834
QY 406 --GTCTTCTGTCGCCAACGACTGGCCTCGCCTGTGTCGCCCTCTCTGTGTGAAGGAGCT 463
DB 835 TAGTCTTTGTTGCCAATGACTGSCACACTGCTCTACTTCCATGTTTACCTCAAACTCTATCT 894
QY 464 ACCAGCCCAAGGGCAGTTTCCACAGGCCAAGTCGGTGTGCTGCTATCCACACATCCGCT 523
DB 895 ATCAATCCCGCGGAGTCTACATGAATGCAAGGTGTGCTTCTGCAATCCACACATAGCCT 954
QY 524 TCCAGGGCGCATGTGGGAGGAGGCTTTCAAGGACACGAAGCTTCCAGGACAGGCGCCCTTTG 583
DB 955 ACCAGGAAGAT-----TGCTTTG 975
QY 584 ACAAGTGGCCTTCTCGGACGGCTATGCCAAGGTTTACACTGAGGCCACCCCATGGAGG 643
DB 976 ATGACTATTCCCTTCTCAACTTGCOCATCAGCTTTAAAAGTTCTTTTCGACTTCATGAGG 1035
QY 644 AGGACGAGAACGCCCGCTGACGGGAAAGACCTACAGAGATCAACTGGCTGAAGGGTG 703
DB 1036 GGTATGAAAAGCC-----AGTAAAGGACGGAATAAATGATGGATGAAGGCTG 1083
QY 704 GCATTATCGCCGCGCAAGCTGGTGTGCTGTGCGCCCAACTACGGACCGGAGATCGCTG 763
DB 1084 CAATCTGGAAGCTTACCGTGTCTTAACAGTTAGTCCATCTACTACGCTCAAGACTCATCT 1143
QY 764 CCGATGCCCGCGGGTGTGGAGCTGGACACCGTCTATCCGCGCCCAAGGCGATTTAGGGCA 823
DB 1144 CTGGAGTTGATAGAGCGGTGGAATTCATAAATATTCGAATGAAACAGATTTCCGGAA 1203
QY 824 TTGTGAACGCGATGGACATTGAGAGTGGAGCGGACCCCAAGACCGACAGTTCTCTGTGCGC 883
DB 1204 TTATTAAATGGAATGGAATTCAGAATGAACCCCGTCTACTGCAAGTACATCGATATCA 1263
QY 884 CCTACACCAAGACAGCGTCTAGCGCGGAAAGCGCCGCCAGAGGAGGCGCTTCAGGCGCG 943
DB 1264 AATACGATATTACCACTGTTACAGATGCTAAACCAATTGATCAAGAAGACACTTCAGGCTG 1323
QY 944 AGCTGGCGCTGCTGTGGACCCCGCCCGCTGTTCGCTTCATCGCGCCCTGAGG 1003
DB 1324 CTGTTGGACTTCCCGTGGACAGGATGTCCCGGTTATCGGTTTCATAGGAGATTTGAGG 1383
QY 1004 AGCAGAGGCTGTGGACATCATCTCGCGCGCTCTGCGCCCAAGATCTCTGGCCACCCCAAG 1063
DB 1384 AGCAGAGGTTCTGATATTCTAGTGAAGCTATTTCRAAGTTTCATGG---GGCTCAATG 1440
QY 1064 TGCAGATCGCCATCTCTGGTACCGCAAGSCCGCTTACGAGAAGCTGGTGAAGCCATCG 1123
DB 1441 TTCAGATGTTATCTCTTGGACTTGAAGAAGAAGATGGAGGCTCAGATTCTTTGAAGTAG 1500
QY 1124 GCACCAAGTACAAAGGCGCGCGCAAGGGGTGTGTAAGTTCTCGGCGCCCTCGGCGACA 1183
DB 1501 AGAGAAGTTCACCAAGGCGGTTGGAGTGGCGGAATTCACAGTGCCATGGCTCATTA 1560
QY 1184 TGCACCGCGCGCGGCTTCATGCTGTGCTGCTTCCGCTTCGAGCCCTCGGCGCTGA 1243
DB 1561 TGATCACTGCTGGAGCTGACTTCATCTATGTTCCAAAGAGGTTTGAAGCGGTGGTCTCA 1620
QY 1244 TCCAGTGCACGCGCATCTACGTTACGTTACCGTGTCCCTGTAGCTTCCACCGCGGCTGG 1303
DB 1621 TTCAGTGCACGCAATGATATGGAACCGTCCCTTATTTGGCATCTACTTGTGGACTTG 1680
QY 1304 TGCACACCGTCAAGAGGCGGTTCACCGGCTTCCACATGGG-----CGCCCTGAACCCG 1357
DB 1681 TGGACACTGTGAAGATGCTACACAGGTTTCCACAGTTTGAAGATTCACGTTCAAGTTG 1740
QY 1358 ACAAGCTGACAGGCTGACGCGGCGCTGCGCGCCACCGTGGCGCGCTGCGCAGGAGG 1417
```

Db 1741 AAGTTGTGGATCCAGATGATGTATGATCAACAGCAAGAGCGCTGTGACAGAGCGCTTGCGAG 1800
QY 1418 TGTTTTGGGGGGCGCGTACCCCGAGATGGTGGCCAACTGCATCAGCCAGGACCTGTCT 1477
Db 1801 TATATGGAACATCCCAATGCAAGAAATGGTCAAGAACTGCATGACCAAGACTTCTCT 1860
QY 1478 GTCCCAAGCGCCGCCAGAGTGGAG 1503
Db 1861 GGAAGGACCTGCGAGGTGTGGAG 1886

RESULT 7
ABK53215
ID ABK53215 standard; cDNA; 2183 BP.
AC ABK53215;
XX
XX
DT 14-AUG-2002 (first entry)
XX
DE Canna edulis granule-bound starch synthase I (GBSSI) cDNA sequence.
XX
KW Starch; amylose; cereal crop; commodity starch; thickened foodstuff;
KW bread; baking; pasta; potato; granule-bound starch synthase I; GBSSI; ss.
XX
XX Canna edulis.
XX
XX WO200218606-A1.
XX
XX 07-MAR-2002.
XX
XX 28-AUG-2000; 2000WO-US23494.
XX
XX 28-AUG-2000; 2000WO-US23494.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Broglie K, Lightner J;
XX
XX WPI; 2002-404556/43.
XX
XX Novel starch isolated from cereal crop with a modification of amylose
XX content and/or amylose weight distribution relative to commodity starch
XX from same species of the cereal crop, for preparing thickened
XX foodstuffs -
XX
XX Example 1; Page 37-38; 44pp; English.
XX
XX The present invention relates to a new starch comprising amylose,
XX where the starch is isolated from a cereal crop, and comprises a 50%
XX increase in average molecular weight relative to commodity starch from
XX the same species of the cereal crop from which starch was isolated.
XX The starch of the invention is useful for preparing thickened foodstuffs
XX by combining the starch, a foodstuff and water and cooking the resulting
XX composition as necessary to produce a thickened foodstuff. The invention
XX is also useful for preparing foodstuffs such as breads, baked goods,
XX pastas, etc. The present nucleic acid sequence represents the Canna
XX edulis granule-bound starch synthase I (GBSSI) cDNA sequence in clone
XX ectlc.pk007.015 that was used in the methods of the invention for
XX generation of a full-length sense Canna edulis GBSSI construct.
XX
XX Sequence 2183 BP; 636 A; 428 C; 516 G; 603 T; 0 other;
XX

Query Match 16.28; Score 258; DB 24; Length 2183;
Best Local Similarity 51.68; Pred. No. 5.1e-32;
Matches 794; Conservative 0; Mismatches 650; Indels 96; Gaps 5;

QY 5 TGGACATCGTATGGTGTCTGCTGAGGTCGCCCTTGTTCCAAAGACGGCGCTGGGCG 64
Db 357 TGAACCTGGGTTTGTGGTGTGAGGTAGCTCCATGAGCAAACTGGGGGCTTGGCG 416
QY 65 ATGTGACTGTGGCTGCTATGAGCTGGTCAAGCGCGGCCACCGGCTCATGACATTG 124
Db 417 ATGTTCTTATAGGATTGCCACCTGCTATGCTGCTGCAATTGGGCACAGGCTCATGCCGTGG 476

QY 125 CCCCTGCTACGACCACTAGCTGACGCTGGGACACCTCGGTGTCGTGGACAT----- 179
Db 477 CGCCAGATATGACCAATATAAAGATATCTGGATACAAGTGTCCAGTTGAGTTAAAG 536
QY 180 -----CATGGCGGAGAGGTCCGCTACTTCACATCCATCAAGAAAGGGGTGCACCGG 232
Db 537 TTGGGATAAGATTGAAACTGTCCGCTTCTCCACTGCTACAAAAGGGAGTTGATCGGG 596
QY 233 TGTGATTGACCAACCCCTGTTCTGGCCAAAGTCTGGGCAAGACCGCTCCAAGCTGT 292
Db 597 TTTTGTGGATCACCTATGTTCTCGAAGAGTTTGGGGGAAACAGGAGGAAATAT 656
QY 293 ACGGCCCGCTCCGCGCTGACTACTGACAAACACAAAGCGCTTCGCCCTGTTCTGCA 352
Db 657 ATGTCCTCTTACAGGAACAGATTATGACAGCAATCAACTAAGATTACGCCITTTGTGCC 716
QY 353 AGCGCGCTATTGAGGTGCCCGGTGCTCCCTTCGGCCCGCGGAGGACTGG----- 405
Db 717 TGGCAGCTCTGGAAGCTCCAAGACTTCTAAATCTCAACACAGCAAAATCTATTCTGAC 776
QY 406 -----GTCCTGTTGGCCAAAGCTGCGCACTCCGCTGGTGGCGCTCC 448
Db 777 CATATGGAGATGATGTTGTTTATGTCACAGATTGGCAATCTGCTCTACTGCCCTGCT 836
QY 449 TGTGAAGGACGAGTACCAGCCCAAGGCGGAGTTCACCAAGGCCAAGTCGGTCTGGGTA 508
Db 837 ACTTGAAGAACTATGTACCAATCACATGATGTTTACATGAATGCTAAGGTTGCAATTGCA 896
QY 509 TCCCAACATCGCTTCCAGGCGCGCATGTGGAGGAGGCTTTCAGAGCACAGAGCTGC 568
Db 897 TTCATAATATGCTTACCAGGCGCGATTTGCCCTTTTCGGAGCTTGAACCTCTTAATCTCC 956
QY 569 CCCAGGCGCGCTTGCACAGCTGGCTTCTCGAGCGGTATGCCAAGGTTTACTACTGAGG 628
Db 957 CCAATAAATTTAAATCTTCATTGATTTCATGATGATATGACAACT----- 1006
QY 629 CCACCCCATGAGGAGGACGAGAGAGCCCGCTGACGGGAAGACCTTACAAGAGATCA 688
Db 1007 -----GTGAAGGAAGGAAATAA 1025
QY 689 ACTGCTGAAGGTGGCATATTCGCGCGCAGCAAGCTGTGACTGTGTCGCCCACTAGG 748
Db 1026 ATTGATGAAGGCTGGATAATAGAAATGTAGTGTGCTGACCGCTGAGCCCATATTATG 1085
QY 749 CGACCGAGATCGCTGCCGATGCCGCGGTGTGAGCTGGACACCGCTCATCCGCGCA 808
Db 1086 CCAAGAGCTTCTCAGGGGTAGAGAAGGGTGTGAGTTGGCAATATCTCTCGCATCA 1145
QY 809 AGGCGATTGAGGGCAATTGTGAAGCGCATGGACATTGAGAGTGGAAACCCCAAGACGACA 868
Db 1146 AAACCATCTGTGGAATAGTAATGGATGGACACCGAGTGGAAATCCATTAAAGACA 1205
QY 869 AGTTCCTGTCTCGCGCTACGACACAGACAGCTGTACGCCGCAAGCGCGCCCAAGG 928
Db 1206 ATATATTCTACAACATACGATGCAACAACTGTATGATGCAAAACCTCTCTGTAAAG 1265
QY 929 AGGCCCTGCAGGCGGAGCTGGCGCTGCCCTGTGGACCCCAACCGCCCTGTTCGCTTCA 988
Db 1266 AAGCTTTCAGCTGAGTGGCTGCCCTGTTTAAACAAACAAAGCTTGTTCGCTTGG 1325
QY 989 TCGGCCGCTGGAGAGCAGAGAGGTGTGGACATCATCTCGCCGCGCTTCCCAAGATCC 1048
Db 1326 TTGAAGACTAGATGAGCAGAAAGGCTCAGACATTTCTAGCTGACGAATTCAGAACTTC 1385
QY 1049 TGGCCACCCCAAGGTGAGATCGCCATCTCGGTACCGGCAAGCGCGCTTACGAGAAGC 1108
Db 1386 T---TTGTGAGAAATTTCAAGTATGATGTTGGCACTGGCAAGAAAGTTGGAGATG 1442
QY 1109 TGGTGAACGCCATCGGCACCAAGTACAAGGCGCGCCCAAGGCGGTGTTCAAGTTCTCGG 1168
Db 1443 AACITACATTACTTGAGGAAATGTTTCCAGACAAATTCAGACCATCTCAAAATCAAG 1502

XX Wheat starch synthase clone wSIIIB cDNA.
XX Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
KW food product; adhesive; ss.
XX Triticum aestivum.
XX OS
XX PN WO200066745-A1.
XX PD 09-NOV-2000.
XX PF 28-APR-2000; 2000WO-AU00385.
XX PR 29-APR-1999; 99AU-0000052.
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PA (GOOD-) GOODMAN FIELDER LTD.
XX PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX PI Morell M, Li Z, Rahman S, Appels R;
XX WPI; 2000-647602/62.
XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and
PT WST-II, useful in modifying plant starch content and/or composition -
XX Disclosure; Fig 2; 21lpp; English.
XX The present invention relates to novel protein and coding sequences from
CC wheat. The proteins are wheat starch synthases, designated SSII and
CC SSIII. These can be used in the modification of plant starch content or
CC composition, and to screen plants to identify mutations which affect
CC starch content and composition. The starch can then be used in food
CC products, such as flour, and in films, coatings, adhesives, building
CC materials and packaging materials.
XX
XX SQ Sequence 2107 BP; 452 A; 566 C; 664 G; 425 T; 0 other;
Query Match 13.4%; Score 214; DB 21; Length 2107;
Best Local Similarity 55.8%; Pred. No. 3.9e-25;
Matches 478; Conservative 0; Mismatches 360; Indels 18; Gaps 3;
QY 687 CAACTGGCTGAAGGTGGCATTATCCCGCCGACAGAGTGGTGCATGTGCGCCCACTA 746
DB 933 CAACTACTTCGCGCGCGCTGAAGATGGCGACAGGTGTGCTGGTGAAGCGCGGTA 992
QY 747 CGGACCGAGATCGTGGCCATCCCGCGCGGTGGAGCTGGACATCATCC---G 803
DB 993 CTTGTGGAGCTGAAGACGGTGGAGCGCGCTGGGGCTTCACGACATCATACGGCAGAA 1052
QY 804 CGCCAAAGGGCATGAGGGCATTGTGAACGCGATGGACATTGAGAGTGAACCCCAAGAC 863
DB 1053 CGACTGAAGACCCCGGCATCTCAACGCGATCGACACATGAGTGAACCCCGAGGT 1112
QY 864 CGACAGTTCCTGTGCGCCCTACGACACAGACAGGTGT-----ACGCGG 911
DB 1113 GGACGCCCACTCAAGTGGCGGCTACACCAACTTCTCCCTGAGGACGCTGGACTCCGG 1172
QY 912 CAAAGCGCGCCCAAGGAGCGCTGGAGCGCGCTGGCGCTGCTGTGGACCCCAACGC 971
DB 1173 CAAAGCGCGCTGAAGAGGCGCTGACGCGAGCTGGCGCTGACGCTCGCGCGACGT 1232
QY 972 CCGCTGTTCGCTTATCGCGCGCTGGAGGACGAGAGGGTGTGACATCATPCCTGGC 1031
DB 1233 GCGCTCTCGCTTATCGCGCGCTGGAGCGGCGAGAGGGCGTGGAGATCATCGCGGA 1292
QY 1032 CGCCCTGCCAAGTCTGCGACCCCAAGGTGCAGATCGCATCTCTGGTACCGCA 1091
DB 1293 CGCCATGCCCTGGATGTG---AGCCAGAGCTGCAGCTGTGTATGTGGCGACCGGG 1349
QY 1092 GCGCGCTAGAGAGTGTGAGCGCATCGGCAACAGTACAAAGGCGCGCGCAAGGG 1151

DB 1350 CCACGACCTGGAGAGCATCTGCGACACTTCGAGCGGGAGCACCACGACAAAGTGGCGG 1409
QY 1152 CPTGGTCAAAGTCTTCGGCGCCCTTGGCGACATGTCACCGCGCGCGCGACTTCATGCT 1211
DB 1410 GTGGGTGGGTTCCTCGTGGCTGCGCACCGGATCACGGGGGCGGACGCGCTCCT 1469
QY 1212 GGTGCGCTCGGCTTCGAGCCCTGCGCGCTGATCAGTGCAGCGCATGCACTACGGTAC 1271
DB 1470 CATGCCCTCCCGTTCGTGCGCTGCGGCTGAACCAAGCTCTACGCCATGGCCTACGGC 1529
QY 1272 CGTGGCCGTGTAGCTCCACCGCGCGCTGTGTCACCGCTCAAGGAGGCGCTCACCGG 1331
DB 1530 CGTCCCGCTGCTGACCGCTGCGCGCTTCAGGGACACGTCGCGCGCTTCACGCCCTT 1589
QY 1332 CTTCCACATGGCGCCCTGAACCCCGACAGCTGGAGGTGACGCGCGACGCCCTGGC 1391
DB 1590 CAACCACTCGGCGCTCGGTGGAGCTTCGACCGCGCGAGCGCACAAAGCTGATCGAGG 1649
QY 1392 CGCCACCGTGGCGCTGCGCGAGAGTGTGCGGCGCGCGCTACCCCGAGATGTGGC 1451
DB 1650 GTCGGGCACTGCTCCGACCTTACCGAGACTTCAAGGAGAGCTGGAGGCGCTCCAGGA 1709
QY 1452 CAACTGCATCAGCCAGGACCTGCTGTCCTCAAGCGCGCGCGAGAGTGGAGGCGCTGCT 1511
DB 1710 GCGCGCATGTCGAGGACTTCAGCTGGAGACGCGCGCGCAAGCTCTACGAGGACGCT 1769
QY 1512 GGAGGAGGTGGTGTAC 1527
DB 1770 CGTCAAGGCCAAGTAC 1785
RESULT 15
AAC86431
ID AAC86431 standard; DNA; 9024 BP.
XX
XX AAC86431;
XX
XX 01-MAR-2001 (first entry)
XX Wheat SSII gene SEQ ID NO: 37.
XX Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
KW food product; adhesive; ds.
XX Triticum tauschii.
XX OS
XX PN WO200066745-A1.
XX PD 09-NOV-2000.
XX PF 28-APR-2000; 2000WO-AU00385.
XX PR 29-APR-1999; 99AU-0000052.
XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX PA (GOOD-) GOODMAN FIELDER LTD.
XX PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX PI Morell M, Li Z, Rahman S, Appels R;
XX WPI; 2000-647602/62.
XX Nucleic acid molecules encoding wheat starch synthase (WST)-I and
PT WST-II, useful in modifying plant starch content and/or composition -
XX Claim 1; Page 195-200; 21lpp; English.
XX The present invention relates to novel protein and coding sequences from
CC wheat. The proteins are wheat starch synthases, designated SSII and
CC SSIII. These can be used in the modification of plant starch content or
CC composition, and to screen plants to identify mutations which affect
CC starch content and composition. The starch can then be used in food
CC products, such as flour, and in films, coatings, adhesives, building

CC materials and packaging materials.

XX
SQ

Sequence 9024 BP; 2228 A; 2386 C; 2216 G; 2193 T; 1 other;

Query Match

Best Local Similarity 13.3%; Score 212.4; DB 21; Length 9024;

Matches 477; Conservative 0; Mismatches 361; Indels 18; Gaps 3;

QY 687 CAACTGGCTGAAGGTGGCATTAATCGCCGCCGACAGCTGGTACTGTGCGCCAACTA 746
| | | | |
Db 7392 CAACTACTTCGCCCGCGGCTGAAGATGGCGACCAAGTTGCTGGTGAGCCCGGGTA 7451
| | | | |
QY 747 CGCGACCGAGATCGCTGCCGATCCGCCGCCGCTGTGGAGCTGGACACCGTATCC---G 803
| | | | |
Db 7452 CTGTGGGAGCTGAAGACGGTGGAGGGCGCTGGGGCTTCACGACATCATACGGCAGAA 7511
| | | | |
QY 804 CGCCAAAGGCAATTGAGGGCAATTGTAAAGCATGAGCATGAGAGTGGAAACCCCAAGAC 863
| | | | |
Db 7512 CGACTGGAAGACCCCGGCATCGTCAACGGCATCGACACATGAGTGGACCCCGAGGT 7571
| | | | |
QY 864 CGACAAGTTCCTGTCTGCGGCCCTACCAACAGAACAGCGTCT-----ACGCCGG 911
| | | | |
Db 7572 GGAGCCCACTCAAGTCCGAGCGGTACACCACTTCCTCTGAGGACGCTGGACTCCGG 7631
| | | | |
QY 912 CAAGCGCCGCCCAAGGAGCGCTCGAGCGCGAGCTGGGCTGCCCTGTGGACCCCAACGC 971
| | | | |
Db 7632 CAAGCGGCAAGTCAAGGAGCGCTCGAGCGGAGCTGGGCTGGGCTGGGCGCCACGT 7691
| | | | |
QY 972 CCCCCTGTTCCGCTTCATCGCGCGCTGAGGAGCAGAAAGGCTGTGGACATCATCTCTGGC 1031
| | | | |
Db 7692 GCCGTGCTCGGCTTCATCGCGCGCTGACGCGCAGAGGCGTGGAGATCATCGCGGA 7751
| | | | |
QY 1032 CGCCCTGCCCAGATCTCGGCCACCCCAAGTGCAGATCGCCATCCTGGGTACCGGCAA 1091
| | | | |
Db 7752 CGCCATGCTCCCTGGTCTG---AGCCAGACGTGACGTGCTGCTGGGACCGCGCG 7808
| | | | |
QY 1092 GGCCGCTACGAGAGCTGCTGAACGCCATCGCACCAAGTACAGGCGCGGCCAAGGG 1151
| | | | |
Db 7809 CCACGACCTGGAGAGCATGCTCGGGCACTTCAGCGGGAGCACCCAGCAAGGTGCGCGG 7868
| | | | |
QY 1152 CGTGTCTAAGTTCCTCGGCGCCCTGGCGCACATGCTCACCGCGCGCGGCTTCATGCT 1211
| | | | |
Db 7869 GTGGTGGGGTTCCTCGCTCGGCTGGCGCACCGGATCACCGCGGGCGGAGCGCTCT 7928
| | | | |
QY 1212 GGTGCTCGCGCTTCGAGCCCTGCGGCTGATCCAGCTGACGCCATGCACTAAGGTAC 1271
| | | | |
Db 7929 CATGCCCTCCCGGTTGAGCGGCTGGGGCTGAACCAAGCTCTACGCCATGGCTACGGCAC 7988
| | | | |
QY 1272 CGTGCCCGTGTAGCTCCACCGCGGCTGTGTCGACACCGCTCAAGGAGGGGTACCCGG 1331
| | | | |
Db 7989 CGTCCCGCTGCTGACGCGCTGTGGCGGCTCAGGGACACCGTGGCGGCTTCGACCCCTT 8048
| | | | |
QY 1332 CTTCCATATGGCGCCCTGAACCCCGACAAGCTGGACGAGGCTGACGCCAGCGCTGGC 1391
| | | | |
Db 8049 CAACCACTCCGGGCTCGGGTGGACCTTCGACCGCGCGAGGCGCACAGCTCATCGAGGC 8108
| | | | |
QY 1392 CGCCACCGTGGCGCTGCGAGCGGCTGTTCCGGGGCGGCTACCCCGAGATGGTGGC 1451
| | | | |
Db 8109 GCTGGGCACTGCTCCCGCACTACCGAGACTTCAAGGAGAGCTGGAGGGCGCTCCAGGA 8168
| | | | |
QY 1452 CAATGCTATCAGCAGACCTGCTGCTGTCACAGCCCGCCCAAGAGTGGAGGGGCTGCT 1511
| | | | |
Db 8169 GCGCGCATGTGCGAGACTTCAGTGGGAGCACCGCCCAAGCTCTACGAGGAGCTGCT 8228
| | | | |
QY 1512 GGAGGAGTGGTGTAC 1527
| | | | |
Db 8229 CGTCAAGGCCAAGTAC 8244

Search completed: June 3, 2003, 10:09:38
Job time : 279.514 secs

This Page Blank (uspto)

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 09:33:29 ; Search time 1554.22 Seconds
(without alignments)
16599.542 Million cell updates/sec

Title: US-09-980-771A-8
Perfect score: 1593
Sequence: 1 gcctggacatcgtgatgtt.....ccgtggcagagatcccc 1593

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	469.8	29.5	473	10	AV640741
2	457.8	28.7	461	10	AV629488
3	454.6	28.5	2147	11	AY109531
4	444.4	27.9	458	10	AY109531
5	400.8	25.2	436	10	AV629117
6	395.6	24.8	511	10	AV394077

7	365.2	22.9	475	10	AW757933
8	351.2	22.0	799	12	BF863935
9	337.8	21.2	418	10	AV644765
10	295.8	18.6	506	10	AV643281
11	278.4	17.5	702	14	BQ248353
12	272.8	17.1	560	10	AV628313
13	267	16.8	393	10	AV631115
14	251.8	15.8	552	10	BE024926
15	250.2	15.7	517	10	AV641583
16	245.6	15.4	726	14	BQ804991
17	244.2	15.3	532	10	AV641989
18	242	15.2	585	14	BQ246366
19	235.8	14.8	513	10	AV631004
20	235.8	14.8	552	10	AV640546
21	234.8	14.7	524	10	AV641724
22	234.2	14.7	500	10	AV642869
23	233	14.6	502	14	BQ814687
24	231.8	14.6	510	10	AV395307
25	230.4	14.5	761	12	BG366176
26	223.8	14.0	540	10	AV642722
27	222.2	13.9	1545	11	AY112448
28	216.6	13.6	773	12	BG351175
29	212	13.3	572	14	BQ245812
30	211.8	13.3	486	10	AV642834
31	211.8	13.3	504	10	AV629198
32	210.8	13.2	502	10	AV644517
33	210.2	13.2	511	10	BE423250
34	209.2	13.1	696	12	BG351920
35	208.8	13.1	495	10	AV642565
36	208.2	13.1	543	14	BQ245428
37	207	13.0	641	14	BQ247154
38	206.8	13.0	522	10	BE423625
39	206.4	13.0	729	12	BG599615
40	200.8	12.6	493	10	AV631838
41	200.2	12.6	2498	11	AY109714
42	200	12.6	631	13	BF531619
43	199.8	12.5	492	10	AV629891
44	198.8	12.5	484	10	AV629266
45	198.8	12.5	489	10	AV629190

ALIGNMENTS

RESULT 1
AV640741
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

AV640741
AV640741
AV640741.1
GI:10784069
EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 473)
Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K., Nakamura,Y. and Tabata,S.
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)

Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuekazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 473
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"

```
/clone="HCL021f06_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/notes="vector: pBluescriptII SK-; Site.1: EcoRI; Site.2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
BASE COUNT      76 a  162 c  146 g  89 t
ORIGIN
Query Match      29.5%; Score 469.8; DB 10; Length 473;
Best Local Similarity 99.6%; Pred. No. 1.1e-77;
Matches 471; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 17 TGGTGTGCTGAGTGCCTTGGTCCAAAGACGGCGGCTGGGATGTGACTGGTG 76
Db 1 TGGTGTGCTGAGTGCCTTGGTCCAAAGACGGCGTCTGGCGATGTGACTGGTG 60
QY 77 GCCTGCTATGAGTGGTCAAGCGGCGCCACCGCGTATGACATGCGCTCGTACG 136
Db 61 GCCTGCTATGAGTGGTCAAGCGGCGCCACCGCGTATGACATGCGCTCGTACG 120
QY 137 ACCAGTAGCTGAGCTGGGACACCTCGGTGGTGGACATCATGGCGGAGAGTCC 196
Db 121 ACCAGTAGCTGAGCTGGGACACCTCGGTGGTGGACATCATGGCGGAGAGTCC 180
QY 197 GCTACTTCCACTCCATCAAGAAGGCGGTGCACCGCGTGTGATTGACACCCCTGGTTCC 256
Db 181 GCTACTTCCACTCCATCAAGAAGGCGGTGCACCGCGTGTGATTGACACCCCTGGTTCC 240
QY 257 TGGCCAGGTCTGGGCAAGACCGGCTCCAAAGCTGTAGGCGCCCGCTCGGCGTACT 316
Db 241 TGGCCAAAGTCTGGGCAAGACCGGCTCCAAAGCTGTAGGCGCCCGCTCGGCGTACT 300
QY 317 ACCTGGACAAACACAGCGCTTCGCCCTTTCTGCAAGCGCGCTATTGAGGCTGCCCGCG 376
Db 301 ACCTGGACAAACACAGCGCTTCGCCCTTTCTGCAAGCGCGCTATTGAGGCTGCCCGCG 360
QY 377 TGCTGCCCTTCGGCCCGCGGAGGACTGCTCTTGGTGGCCAAAGCTGGCACTCCGCC 436
Db 361 TGCTGCCCTTCGGCCCGCGGAGGACTGCTCTTGGTGGCCAAAGCTGGCACTCCGCC 420
QY 437 TGCTGCCCTTCCTGTAAGACAGTACCAAGCCCAAGGCCAGTTCACCAAG 489
Db 421 TGCTGCCCTTCCTGTAAGACAGTACCAAGCCCAAGGCCAGTTCACCAAG 473

RESULT 2
AV629488 461 bp mRNA linear EST 15-DEC-2000
LOCUS
DEFINITION Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas
reinhardtii cDNA clone LCL059f09_r 5', mRNA sequence.
ACCESSION AV629488
VERSION AV629488.1 GI:10792122
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
1 (bases 1 to 461)
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
Location/Qualifiers
1..461
/organism="Chlamydomonas reinhardtii"
```

```
/strain="C9"
/db_xref="taxon:3055"
/clone="LCL059f09_r"
/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/notes="vector: pBluescriptII SK-; Site.1: EcoRI; Site.2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
BASE COUNT      73 a  156 c  143 g  89 t
ORIGIN
Query Match      28.7%; Score 457.8; DB 10; Length 461;
Best Local Similarity 99.6%; Pred. No. 1.1e-75;
Matches 459; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 ACATCGTATGCTGCTGCTGAGTCCGCCCTTGGTCCAAAGACGGCGGCTGGGCGATG 67
Db 1 ACATCGTATGCTGCTGCTGAGTCCGCCCTTGGTCCAAAGACGGCGGCTGGGCGATG 60
QY 68 TGACTGGTGGCTGCTGCTATGAGCTGGTCAAGCGGCGCCACCGCGTCTATGACCAITGCC 127
Db 61 TGACTGGTGGCTGCTGCTATGAGCTGGTCAAGCGGCGCCACCGCGTCTATGACCAITGCC 120
QY 128 CTCGTAGCACAGTACGCTGACGCTGGGACACCTCGTGGTGGTGGACATCATGGGCG 187
Db 121 CTCGTAGCACAGTACGCTGACGCTGGGACACCTCGTGGTGGTGGACATCATGGGCG 180
QY 188 AGAAGTCCGCTACTTCCACTCCATCAAGAAGGCGGTGCACCGCGTGTGATTGACCA 247
Db 181 AGAAGTCCGCTACTTCCACTCCATCAAGAAGGCGGTGCACCGCGTGTGATTGACCA 240
QY 248 COTGTTCTCTGSCCAAGTCTGGGCAAGACCGGCTCCAAAGCTGTACGCGCCCGCTCGG 307
Db 241 COTGTTCTCTGSCCAAGTCTGGGCAAGACCGGCTCCAAAGCTGTACGCGCCCGCTCGG 300
QY 308 GCGCTGACTACTCTGACACACACACCGCTTCGCCCTTCTGCAAGCGCGCTATTGAGG 367
Db 301 GCGCTGACTACTCTGACACACACACCGCTTCGCCCTTCTGCAAGCGCGCTATTGAGG 360
QY 368 CTGCCCGGCTGTCGCCCTTCGCCCGCGGAGGACTGCGTCTTCGTGGCCAAAGCTG 427
Db 361 CTGCCCGGCTGTCGCCCTTCGCCCGCGGAGGACTGCGTCTTCGTGGCCAAAGCTG 420
QY 428 ACTCGGCCCTGTCGCCCGCTGCTGCTGAAGGACGAGTACCAG 468
Db 421 ACTCGGCCCTGTCGCCCGCTGCTGCTGAAGGACGAGTACCAG 461

RESULT 3
AY109531 2147 bp mRNA linear HTC 25-MAY-2002
LOCUS
DEFINITION Zea mays CL1198_1 mRNA sequence.
ACCESSION AY109531
VERSION AY109531.1 GI:21213285
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2147)
TITLE Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Design of
Maize Mapping Project/DuPont Consensus Sequences for
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 2147)
AUTHORS Coe, E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES
Location/Qualifiers
```


Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 458
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"

BASE COUNT 91 a 147 c 146 g 74 t

Query Match 27.9%; Score 444.4; DB 10; Length 458;
Best Local Similarity 99.6%; Pred. No. 5.8e-73;
Matches 456; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 365 AGGCTGCCCGCTGCTGCCCTTGGCCCGGCGGAGGAGTCTCTGTCGCGCAAGCACT 424
DB 1 AGGCTGCCCGCTGCTGCCCTTGGCCCGGCGGAGGAGTCTCTGTCGCGCAAGCACT 60
QY 425 GGCACCTCCGCTGCTGCCCTTGGCTGAAGGACGAGTACCAGCCCAAGGGCCAGTTCA 484
DB 61 GGCACCTCCGCTGCTGCCCTTGGCTGAAGGACGAGTACCAGCCCAAGGGCCAGTTCA 120
QY 485 CCAAGGCCAAGTGGTGGTATC-CACACATGCGCTTCCAGGGCCGCGATGGGGAG 543
DB 121 CCAAGGCCAAGTGGTGGTATCGCACACATGCGCTTCCAGGGCCGCGATGGGGAG 180
QY 544 GAGGCTTTCAAGGACGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 603
DB 181 GAGGCTTTCAAGGACGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 604 GGTATGCCAAGTGTACACTGAGGCGACCCCATGAGGAGGAGGAGGAGGAGGAGGAGG 663
DB 241 GGTATGCCAAGTGTACACTGAGGCGACCCCATGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 664 ACGGAAAGACCTACAAGAGATCACTGGCTGAAGGGTGGATTTATCGCGCGCGACAAG 723
DB 301 ACGGAAAGACCTACAAGAGATCACTGGCTGAAGGGTGGATTTATCGCGCGCGACAAG 360
QY 724 CTGCTGACGTGTGCGCCCAACTACGGACCGAGATCGCTGCCATGCCCGCGCGGTGTG 783
DB 361 CTGCTGACGTGTGCGCCCAACTACGGACCGAGATCGCTGCCATGCCCGCGCGGTGTG 420
QY 784 GAGCTGGACACCGTATCCCGCGCCCAAGGGCAATTGAGGG 821
DB 421 GAGCTGGACACCGTATCCCGCGCCCAAGGGCAATTGAGGG 458

RESULT 5
AV629117
LOCUS
DEFINITION AV629117 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas
reinhardtii cDNA clone LCL052d05_r 5', mRNA sequence.
ACCESSION AV629117
VERSION AV629117.1 GI:10791751
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
REFERENCE 1 (bases 1 to 436)
AUTHORS Asamizu, Y., Miura, K., Kuchio, K., Inoue, Y., Fukuzawa, H., Ohya, K.,
Nakamura, Y., and Tabata, S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)

205399644

MedLINE
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
1. 436
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"

FEATURES
source

BASE COUNT 66 a 145 c 138 g 87 t

Query Match 25.2%; Score 400.8; DB 10; Length 436;
Best Local Similarity 99.5%; Pred. No. 7.4e-65;
Matches 402; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGCCTGGACATCGTATGTTGCTGCTGAGTGGCCCTTGGTCCAGACGGCGGCTG 60
DB 33 GGCCTGGACATCGTATGTTGCTGCTGAGTGGCCCTTGGTCCAGACGGCGGCTG 92
QY 61 GCGATGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
DB 93 GCGATGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 152
QY 121 ATTGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 153 ATTGCCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 212
QY 181 ATGGGCGAGAAGTCCGCTACTTCCACTCCATCAAGAGGGCGTGCACCGGCTGGATT 240
DB 213 ATGGGCGAGAAGTCCGCTACTTCCACTCCATCAAGAGGGCGTGCACCGGCTGGATT 272
QY 241 GACCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 273 GACCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 332
QY 301 CGCTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 333 CGCTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 392
QY 361 ATTGAGGCTGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 404
DB 393 ATTGAGGCTGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 436

RESULT 6
AV394077
LOCUS
DEFINITION AV394077 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
cDNA clone CL18c08_r 5', mRNA sequence.
ACCESSION AV394077
VERSION AV394077.1 GI:6548293
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
REFERENCE 1 (bases 1 to 511)
AUTHORS Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H., and Tabata, S.
TITLE A large scale structural analysis of cDNAs in a unicellular green
alga, Chlamydomonas reinhardtii. I. Generation of 3433
non-redundant expressed sequence tags
JOURNAL DNA Res. 6 (6), 369-373 (1999)
MEDLINE 20152988

TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 3

JOURNAL Unpublished (2000)

COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES Location/Qualifiers
source
1..799
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
normalized, lambda zap II"
/note="vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min,
1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, 1hr
, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda Zap II
(Stratagene) in the EcoRI (5') and XhoRI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

BASE COUNT 141 a 256 c 208 g 193 t 1 others

ORIGIN

Query Match 22.0%; Score 351.2; DB 12; Length 799;
Best Local Similarity 98.9%; Pred. No. 1.4e-55;
Matches 364; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1155 GGTCAAGTCTTCGGCGCCCTGGCGCACATGCTACCGCGCGCGGCTTCATGCTGGT 1214
Db 124 GGTCAAGTCTTCGGCGCCCTGGCGCACATGCTACCGCGCGCGGCTTCATGCTGGT 183

Qy 1215 GCCCTCGCGCTTCGAGCCCTCGGGCTGATCCAGTGCACGCCATGACTACGGTACCGT 1274
Db 184 GCCCTCGCGCTTCGAGCCCTCGGGCTGATCCAGTGCACGCCATGACTACGGTACCGT 243

Qy 1275 GCCCTCGGTAGCTCCACCGGGGCTGGTGCACACCGTCAAGAGGGGCTCAACCGGCTT 1334
Db 244 GCCCTCGGTAGCTCCACCGGGGCTGGTGCACACCGTCAAGAGGGGCTCAACCGGCTT 303

Qy 1335 CCACATGGCGCCCTGAACCCCGACAAAGCTGGACGAGGCTGACGCGCGCGCCCTGGCGCG 1394
Db 304 CCACATGGCGCCCTGAACCCCGACAAAGCTGGACGAGGCTGACGCGCGCGCCCTGGCGCG 363

Qy 1395 CACCTGCGCGCTGCCAGGAGGTGTTTGGGGGCGCGCTTACCCCGAGATGGTGGCCAA 1454
Db 364 CACCTGCGCGCTGCCAGGAGGTGTTTGGGGGCGCGCTTACCCCGAGATGGTGGCCAA 423

Qy 1455 CTGCATCAGCCAGGACCTGCTCTGCTCCAAAGCCCGCCAGAGTGGAGGGCC-TGCTGG 1513
Db 424 CTGCATCAGCCAGGACCTGCTCTGCTCCAAAGCCCGCCAGAGTGGAGGGCC-TGCTGG 483

Qy 1514 AGGAGGTG 1521

Db 484 AGGAGGTG 491

RESULT 9
AV644765 418 bp mRNA linear EST 15-DEC-2000
LOCUS
DEFINITION AV644765 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
CDNA clone HCL093d12_r 5', mRNA sequence.

ACCESSION AV644765

VERSION AV644765.1 GI:10788093

KEYWORDS EST.

SOURCE Chlamydomonas reinhardtii.

ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 418)
AUTHORS Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii

TITLE DNA Res. 7 (5), 305-307 (2000)

JOURNAL 20539644

MEDLINE

COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES Location/Qualifiers
source
1..418
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone_lib="HCL093d12_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"

BASE COUNT 65 a 139 c 130 g 84 t

ORIGIN

Query Match 21.2%; Score 337.8; DB 10; Length 418;
Best Local Similarity 99.4%; Pred. No. 3.8e-53;
Matches 339; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGCCTGGACATCGTATGTTGCTGCTGAGTGCCTTGTTCCTCAAGACGGCGGCTCG 60
Db 78 GGCCTGGACATCGTATGTTGCTGCTGAGTGCCTTGTTCCTCAAGACGGCGGCTCG 137

Qy 61 GCGATGTGACTGGTGGCTGCTATTGAGCTGGTCAAGCGGGCCACCGCGTCAATGACC 120
Db 138 GCGATGTGACTGGTGGCTGCTATTGAGCTGGTCAAGCGGGCCACCGCGTCAATGACC 197

Qy 121 ATTGCCCTCGCTACGACCAAGTACGCTGACGCTGCGCTGCGACACCTCGGTGGTGGACATC 180
Db 198 ATTGCCCTCGCTACGACCAAGTACGCTGACGCTGCGCTGCGACACCTCGGTGGTGGACATC 257

Qy 181 ATGGGGGAGAAAGTCCGCTACTTCCACTCCATCAAGAGGGGTGCACCGGTGTGATT 240
Db 258 ATGGGGGAGAAAGTCCGCTACTTCCACTCCATCAAGAGGGGTGCACCGGTGTGATT 317

Qy 241 GACCAACCCCTGGTTCCTGGCCAAAGTCTGGGGCAAGACCGGCTCCAAAGTGTACGGCCCC 300
Db 318 GACCAACCCCTGGTTCCTGGCCAAAGTCTGGGGCAAGACCGGCTCCAAAGTGTACGGCCCC 377

Qy 301 CGCTCGGCGCTGACTTACCTGGACACCAACCAAGCGCTTCGC 341
Db 378 CGCTCGGCGCTGACTTACCTGGACACCAACCAAGCGCTTCGC 418

RESULT 10
AV643281 506 bp mRNA linear EST 15-DEC-2000
LOCUS
DEFINITION AV643281 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
CDNA clone HCL066h09_r 5', mRNA sequence.

ACCESSION AV643281

VERSION AV643281.1 GI:10786609

KEYWORDS EST.

SOURCE Chlamydomonas reinhardtii.

ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

REFERENCE

1 (bases 1 to 506)
 Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K., Nakamura,Y. and Tabata,S.
 Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of *Chlamydomonas reinhardtii*
 DNA Res. 7 (5), 305-307 (2000)
 20539644
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizuekazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

source

1. 506
 /organism="Chlamydomonas reinhardtii"
 /strain="C9"
 /db_xref="taxon:3055"
 /clone_lib="HCL06h09_r"
 /clone_lib="Chlamydomonas reinhardtii 5% CO2"
 /note="Vector: pBluescriptII SK; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from cells cultured in a medium with bubbling air containing 5% carbon dioxide"

BASE COUNT 77 a 170 c 160 g 99 t
 ORIGIN

Query Match 18.6%; Score 295.8; DB 10; Length 506;
 Best Local Similarity 99.3%; Pred. No. 2.5e-45;
 Matches 297; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCCTGGACATCGTGATGGTGTGCTGAGTGGCCCTTGGTCCAGAGCGGCGGCTG 60
 Db 208 GCCTGGACATCGTGATGGTGTGCTGAGTGGCCCTTGGTCCAGAGCGGCGGCTG 267
 QY 61 GCGCATGTGACTGGTGGCTGCTATTGAGTGGTCAAGCGGCCACCGCTCATGACC 120
 Db 268 GCGCATGTGACTGGTGGCTGCTATTGAGTGGTCAAGCGGCCACCGCTCATGACC 327
 QY 121 ATTGCCCTCGCTACACAGTAGTACGCTGAGCGCTGGACACCTCGGTGGTGGACATC 180
 Db 328 ATTGCCCTCGCTACACAGTAGTACGCTGAGCGCTGGACACCTCGGTGGTGGACATC 387
 QY 181 ATGGGGGAGAAGTCCGCTACTTCCACTCCATCAAGAAGGCGGTGCACCGCTGGATT 240
 Db 388 ATGGGGGAGAAGTCCGCTACTTCCACTCCATCAAGAAGGCGGTGCACCGCTGGATT 447
 QY 241 GACCACCCCTGGTCTCTGCGCAAGGTCTGGGGCAAGACCGGCTCCAAAGCTGTACGGCC 299
 Db 448 GACCACCCCTGGTCTCTGCGCAAGGTCTGGGGCAAGACCGGCTCCAAAGCTGTACGGCC 506

RESULT 11

BQ246353

LOCUS

DEFINITION BQ246353 702 bp mRNA linear EST 03-MAY-2002
 Tae15012H04R Tae15 Triticum aestivum cDNA clone Tae15012H04R, mRNA sequence.

ACCESSION

BQ246353

VERSION

BQ246353.1

KEYWORDS

EST.

SOURCE

bread wheat.

ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Triticum.
 1 (bases 1 to 702)

REFERENCE

AUTHORS

Cloutier, S.

TITLE

Wheat functional genomics - Glenlea developing seeds cDNA libraries

JOURNAL

Unpublished (2002)

COMMENT Contact: Dr. Sylvie Cloutier
 Cereal Research Centre, Agriculture and Agri-food Canada
 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
 Tel: (204) 983-2340
 Fax: (204) 983-4604

FEATURES

source

Email: scloutier@em.agr.ca
 was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
 Average insert size is >1.4 kb
 Plate: 012 row: H column: 04
 Seg primer: M13 Reverse.
 Location/Qualifiers
 1. 702
 /organism="Triticum aestivum"
 /cultivar="Glenlea"
 /db_xref="taxon:4565"
 /clone="Tae15012H04R"
 /clone_lib="Tae15"
 /tissue_type="developing seeds"
 /dev_stage="15 days after anthesis"
 /lab_host="E. coli DH10B"
 /note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies); Site_1: NotI; Site_2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 15 days post-anthesis"
 BASE COUNT 143 a 213 c 237 g 109 t
 ORIGIN

Query Match 17.5%; Score 278.4; DB 14; Length 702;
 Best Local Similarity 66.5%; Pred. No. 4.6e-42;
 Matches 399; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
 QY 682 AAGATCAACTGGCTGAAGGGTGGCATTTATCGCGCCGACAGCTGGTGACTGTGTGCGCC 741
 Db 103 AAGATCAACTGGATGAAGCGCGGATCTCGAGGCCGACAGAGTGTGACGGTGAAGCC 162
 QY 742 AACTACCGACCGAGATCGCTGCGCATGCGCGCGCGGTGTGGAGCTGGACACCGTCATC 801
 Db 163 TACTACCGAGGAGCTCATCTCTGCGGAAGCCAGGGCTGCGAGCTCGACAACATCATG 222
 QY 802 CGGCCCAAGGSCATTTAGGGCATTTGTAACGGCATGACATTTAGGAGTGGAAACCCCAAG 861
 Db 223 CGCTCTACTGGGATCACCGCATGCTCAACGGCATGATGTAGCGAGTGGGAGCCCAACC 282
 QY 862 ACGGACAAGTTCTCTGTCGCGCTTACGACCAAGACAGCGCTCTACGCGCAAGCGCGCC 921
 Db 283 AAGGACAAGTTCTCTGCGCTTCACTAGACATCACACCGCTTGGAGGGAAGCGCGCTG 342
 QY 922 GCCAAGAGCGCTTGCAGCGCGAGCTGGGCTGTGAGACCCGCCGCCGCCCTTTC 981
 Db 343 AACAAAGAGCGCTTGCAGCGCGAGTGGGCTGCGGTGGAGCAAGGTGCCCCCTGGTG 402
 QY 982 GCCTTCATCGCGCCCTGGAGGAGCAAGAGGTGTGACATCATCTTGGCGCGCCCTGCC 1041
 Db 403 GCCTTCATCGCGAGCTTGGAGGAGCAAGAGGCGCCGACGTGATCGCGCCCATCCG 462
 QY 1042 AAGATCTTGGCCACCCCAAGGTGCAGATCGCATCTGGGTACCGGCAAGCGCGCTAC 1101
 Db 463 GAGATCTTGAAGGAGGAGGAGCTCCAGATGTTCTTCTGCGCACCGGGAAGAAGAGTTC 522
 QY 1102 GAGAAGTGTGTAAAGCCCATTCGACACCAAGTACAAGGCGCCGCCCAAGGCGGTGTCAG 1161
 Db 523 GAGCGGCTACTCAAGAGCATTTAGAGGAAATTTCCGAGCAAGGTGAGGGCGGTGTCAGG 582
 QY 1162 TTCTCGGCGCCCTGGGCGACATGCTCACGCGCGCGCGCACTTCATGCTGGTGGCCCTCG 1221
 Db 583 TTCAACGCGCGCTGGCTCACCAGATGATGGCGCGCGGACGTGCTCGCGCTCAACAGC 642
 QY 1222 CGCTTCGAGCCCTTGGCGCTGTATCCAGCTGCACGCCCATGACCTACCTACCGTGGCCGCTG 1281
 Db 643 CGCTTCGAGCCCTTGGCGCTTATCCAGCTCCAGGGGATGCGCTTACGGAACGCGGTGCGG 702

RESULT 12

AV628313

LOCUS

DEFINITION

AV628313 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LCL039h11_r 5', mRNA sequence.

ACCESSION

AV628313

```
VERSION AV628313.1 GI:10790947
SOURCE EST.
ORGANISM Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 560)
AUTHORS Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
Location/Qualifiers
1..560
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="ICL039h11_r"
/note="Vector: pBluescriptII SK-; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
BASE COUNT 92 a 186 c 173 g 109 t
ORIGIN
Query Match 17.1%; Score 272.8; DB 10; Length 560;
Best Local Similarity 99.3%; Pred. No. 4.9e-41; Indels 0; Gaps 0;
Matches 274; Conservative 0; Mismatches 2;
QY 1 GCGCTGGACATCGTGGTGTCTGCTGAGGTGCGCCCTTGGTCCAAAGACGGCGCGCTG 60
DB 285 GCGCTGGACATCGTGGTGTCTGCTGAGGTGCGCCCTTGGTCCAAAGACGGCGCTG 344
QY 61 GCGATGTGACTGTGGTGGCTGCTGTAGCTGTGTCACGGCGGGCCACCGGTGATGACC 120
DB 345 GCGATGTGACTGTGGTGGCTGCTGTAGCTGTGTCACGGCGGGCCACCGGTGATGACC 404
QY 121 ATTGCCCTCGCTAGACAGTACGTGACGCTGGGACACCTCGGTGTGCTGGACATC 180
DB 405 ATTGCCCTCGCTAGACAGTACGTGACGCTGGGACACCTCGGTGTGCTGGACATC 464
QY 181 ATGGCGAGAGTCCGCTACTTCCACTCCATCAAGAGGGCGGTGACCGCGTGTGGATT 240
DB 465 ATGGCGAGAGTCCGCTACTTCCACTCCATCAAGAGGGCGGTGACCGCGTGTGGATT 524
QY 241 GACCACTCCCTGCTTCTGCGCAAGTCTGGGCAAG 276
DB 525 GACCACTCCCTGCTTCTGCGCAAGTCTGGGCAAG 560
RESULT 13
LOCUS AV631115 393 bp mRNA linear EST 15-DEC-2000
DEFINITION AV631115 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas
reinhardtii cDNA clone ICL089a12_r 5', mRNA sequence.
ACCESSION AV631115
VERSION AV631115.1 GI:10793749
KEYWORDS EST.
ORGANISM Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 393)
AUTHORS Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
Location/Qualifiers
1..393
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="ICL089a12_r"
/note="Vector: pBluescriptII SK-; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
BASE COUNT 64 a 145 c 137 g 47 t
ORIGIN
Query Match 16.8%; Score 267; DB 10; Length 393;
Best Local Similarity 100.0%; Pred. No. 5.5e-40;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1327 ACCGGCTTCCACATGGCGCCCTGAACCCGCAACGCTGACGAGGCTGACGCCGACGCC 1386
DB 1 ACCGGCTTCCACATGGCGCCCTGAACCCGCAACGCTGACGAGGCTGACGCCGACGCC 60
QY 1387 CTGGCGCCACCGTGGCGGTGCGGAGGTGTTTTCGGGGCGGCGCTACCCCGAGATG 1446
DB 61 CTGGCGCCACCGTGGCGGTGCGGAGGTGTTTTCGGGGCGGCGCTACCCCGAGATG 120
QY 1447 GTGGCCAACTGATCAGCAGGACCTGCTCTGTGTCACAGCCGCCAGAGTGGAGGCC 1506
DB 121 GTGGCCAACTGATCAGCAGGACCTGCTCTGTGTCACAGCCGCCAGAGTGGAGGCC 180
QY 1507 CTGCTGGAGAGGTGTGTACGCAAGGGCGGCTGGCCACCCCAAGAGAGGAGATC 1566
DB 181 CTGCTGGAGAGGTGTGTACGCAAGGGCGGCTGGCCACCCCAAGAGAGGAGATC 240
QY 1567 AAGTGCCCGCTTCCCGAGAGATCCCC 1593
DB 241 AAGTGCCCGCTTCCCGAGAGATCCCC 267
RESULT 14
LOCUS BE024926 552 bp mRNA linear EST 06-JUN-2000
DEFINITION BE024926 894006H08.y1 C. reinhardtii CC-1690, normalized, Lambda zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BE024926
VERSION BE024926.1 GI:8287367
KEYWORDS EST.
ORGANISM Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 552)
AUTHORS Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.
ANALYSES Analysis of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants: project phase 2
JOURNAL Unpublished (2000)
COMMENT Contact: Elizabeth H. Harris
DCMB Box 91000
Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
```

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan

Search completed: June 3, 2003, 15:27:33
Job time : 1560.22 secs

This Page Blank (uspto)

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 09:49:44 ; Search time 38.3196 Seconds
(without alignments)
12748.991 Million cell updates/sec

Title: US-09-980-771A-8

Perfect score: 1593

Sequence: 1 gcgcgtgacatcgatggt.....ccgttgccgagaagatcccc 1593

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA:*

- 1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2.6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2.6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2.6/ptodata/1/ina/PCTUS.COMB.seq:*
- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	474.8	29.8	2267	4	US-08-679-645-25
2	447.4	28.1	2542	3	US-08-941-445A-6
3	276.2	17.3	2067	4	US-09-388-743-21
4	266.6	16.7	2274	4	US-09-388-743-17
5	259.6	16.3	2176	4	US-09-388-743-13
6	255.4	16.0	2202	4	US-09-388-743-1
7	218.2	13.7	2825	4	US-09-196-390-5
8	216.8	13.6	2097	3	US-08-941-445A-10
9	210.2	13.2	2380	1	US-08-572-951-3
10	207	13.0	2248	4	US-09-345-214-20
11	206.6	13.0	1798	4	US-09-345-214-16
12	206.6	13.0	2019	4	US-09-345-214-15
13	161	10.1	2007	3	US-08-941-445A-8
14	161	10.1	2085	1	US-08-572-951-2
15	118.2	7.4	2239	4	US-09-196-390-1
16	109.6	6.9	2348	4	US-09-388-743-5
17	108	6.8	1758	3	US-08-836-567-3
18	106.8	6.7	2418	4	US-09-388-743-25
19	106.6	6.7	2360	3	US-08-836-567-9
20	102.6	6.4	1528	4	US-09-345-214-6
21	102.6	6.4	1620	3	US-08-941-445A-20
22	102.6	6.4	1752	3	US-08-941-445A-12
23	102.6	6.4	2008	4	US-09-345-214-12
24	102.6	6.4	2491	4	US-09-345-214-5
25	101	6.3	2383	4	US-09-192-909-1
26	97.8	6.1	2990	1	US-08-572-951-1
27	97.4	6.1	4800	3	US-08-941-445A-4

28	96.4	6.1	2277	1	US-08-676-967-5	Sequence 5, Appli
29	96.4	6.1	2277	1	US-08-676-974-5	Sequence 5, Appli
30	96.4	6.1	2277	2	US-09-098-487-5	Sequence 5, Appli
31	89.2	5.6	2793	3	US-08-836-567-7	Sequence 7, Appli
32	88.4	5.5	6027	2	US-08-968-542C-1	Sequence 1, Appli
33	84.4	5.3	1926	3	US-08-836-567-5	Sequence 5, Appli
34	82.6	5.2	1464	1	US-07-735-065-1	Sequence 1, Appli
35	82.6	5.2	1464	1	US-08-469-202-11	Sequence 11, Appli
36	82.6	5.2	1464	2	US-08-484-434C-11	Sequence 11, Appli
37	81.2	5.1	2809	3	US-09-000-016-1	Sequence 1, Appli
38	81.2	5.1	2809	4	US-09-514-340-1	Sequence 1, Appli
39	79.6	5.0	2539	3	US-09-000-016-3	Sequence 3, Appli
40	79.6	5.0	2539	4	US-09-514-340-3	Sequence 3, Appli
41	78.4	4.9	2549	1	US-08-470-720-2	Sequence 2, Appli
42	78.4	4.9	4964	1	US-08-470-720-5	Sequence 5, Appli
43	77	4.8	44377	1	US-08-804-227C-7	Sequence 7, Appli
44	77	4.8	44377	2	US-08-804-198-1	Sequence 1, Appli
45	74.4	4.7	2712	3	US-09-025-691-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-679-645-25
; Sequence 25, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:										
; LENGTH: 2267 base pairs										
; TYPE: nucleic acid										
; STRANDEDNESS: single										
; TOPOLOGY: linear										
US-08-679-645-25										
Query Match 29.8%; Score 474.8; DB 4; Length 2267;										
Best Local Similarity 59.9%; Pred. No. 6.7e-80;										
Matches 978; Conservative 0; Mismatches 557; Indels 99; Gaps 7;										
QY	5	TGGACATCGT	GATGTTCT	GTCTGCT	AGTGC	CGCCCT	TGTC	CAAGAC	GGCGGCGG	64
DB	418	TGAACGTCGT	TTCTCGT	CGCGCG	AGAGT	GGCGCG	CTGT	GGAGAA	AGACCGCGGCT	477
QY	65	ATGTGACT	GGTGGCT	GCTATT	GAGCT	GTGT	CAAC	CGCGGC	ACCGCTCAT	124
DB	478	ACGTCTCT	CGGGGCT	GTGGCG	CGCAT	GTGGCG	GAAT	GGGCAC	CGGTGTC	537
QY	125	CCCTTCGT	AGACAGT	ACGTC	AGCGCT	GGGAC	ACCT	TCGGT	GTGTCG	179
DB	538	CTCCCGCT	TACGACAGT	TACAGAG	CGCT	GGGAC	ACAG	CGCT	GTGTCG	597
QY	180	-----CAT	GGCGAG	AGGT	TCGCT	ACTT	CCACT	TCAT	CAAGAG	232
DB	598	TGGGAGAC	AGGTAC	GAGCGT	CAGGTT	CTCC	ACT	GTCT	TACAA	657
QY	233	TGTGAT	TGACCA	CCCTG	CTT	GGCG	CAAG	GTCT	GGGCA	292
DB	658	TGTTGTT	GTACCA	CCCTG	CTT	GGCG	CAAG	GTCT	GGGCA	717
QY	293	ACGGCCCC	CGCTTC	CGCGCT	GTACT	ACCT	GGGCA	CAAC	CAAGCG	352
DB	718	ACGGCCCC	CGCTTC	CGCGCT	GTACT	ACCT	GGGCA	CAAC	CAAGCG	777
QY	353	AGGCGCTA	TGAGGT	GC	CGCGT	GTCT	GGCG	CAAG	GTCT	390
DB	778	AGGCGCACT	TGAGGT	GC	CGCGT	GTCT	GGCG	CAAG	GTCT	837
QY	391	--CCGCGG	CAGACT	TCGCT	TCGCT	TCGCT	TCGCT	TCGCT	TCGCT	448
DB	838	CATACGGG	AGGAGC	GTCT	TCGCT	TCGCT	TCGCT	TCGCT	TCGCT	897
QY	449	TGCTGAAG	ACGAGT	ACACCG	CGCGT	GTCT	TCGCT	TCGCT	TCGCT	508
DB	898	ACCTAAG	ACGAGT	ACACCG	CGCGT	GTCT	TCGCT	TCGCT	TCGCT	957
QY	509	TCACAAAT	CGCTTC	CAAGCG	CGCGT	GTCT	TCGCT	TCGCT	TCGCT	568
DB	958	TCACAAAT	CGCTTC	CAAGCG	CGCGT	GTCT	TCGCT	TCGCT	TCGCT	1017
QY	569	CCGAGCGC	CTTTC	CAAGCT	GGCGT	TCGCT	TCGCT	TCGCT	TCGCT	628
DB	1018	CGGAGAGT	CAAGCT	GGCGT	TCGCT	TCGCT	TCGCT	TCGCT	TCGCT	1064
QY	629	CCACCCCA	TGAGG	AGGAG	AGAG	ACCG	CGCGT	GTCT	TCGCT	688
DB	1065	-----CCG	GTGGAG	-----	-----	-----	-----	-----	-----	1086
QY	689	ACTGGCTG	AGGAGT	GGCGT	TCGCT	TCGCT	TCGCT	TCGCT	TCGCT	748
DB	1087	ACTGGATG	AGGAGT	GGCGT	TCGCT	TCGCT	TCGCT	TCGCT	TCGCT	1146
QY	749	CGACCGAT	CGCTTC	CGCGG	CGCGT	GTCT	TCGCT	TCGCT	TCGCT	808
DB	1147	CGGAGGCT	CACTTC	CGCGG	CGCGT	GTCT	TCGCT	TCGCT	TCGCT	1206
QY	809	AGGCAATG	AGGAGT	GGCGT	TCGCT	TCGCT	TCGCT	TCGCT	TCGCT	868
DB	1207	CGGCAATG	AGGAGT	GGCGT	TCGCT	TCGCT	TCGCT	TCGCT	TCGCT	1266
QY	869	AGTTCGCT	GTGGCG	CTTAC	CAAG	AGG	AGG	AGG	AGG	928

RESULT 2

US-08-941-445A-6

Sequence 6, Application US/08941445A

Patent No. 6107060

GENERAL INFORMATION:

APPLICANT: Keeling, Peter

APPLICANT: Guan, Hanning

TITLE OF INVENTION: Starch Encapsulation

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle

CITY: Boulder

STATE: CO

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Parentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

RESULT 2
US-08-941-445A-6
; Sequence 6, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:


```

; APPLICANT: Singletary, George
; APPLICANT: Zhou, Lan
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 2067
; TYPE: DNA
; ORGANISM: Tulipa fosteriana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (58)...(1857)
; US-09-388-743-21

```

QY	745	TACGCCACCGAGATCGCTCCCGATCGCCGCCGCGTGTGGAGCTGGACACCGTCATCCGC	804
Db	1000	TATGCTAAAGACGTCGTCTCTCGGAAGATAGAGGTGCGAGTTGGACACGCTGCTCGGC	1059
QY	805	GCCAAAGGCATTGAGGGCATTTGAAACGCGATGGACATTGAGGAGTGGAAACCCCAAGACC	864
Db	1060	TTGAGGGGGCTCAAGGAATTTGTGAATGGATGGATACATATGTGTGGATCCATTGACA	1119
QY	865	GACAAATTCCTGTCTGCGCCCTACGACCAAGACAGCGCTTACGCCGGCAAGGCGCGCC	924
Db	1120	GACAAATTTTACCTGCAAAATACGATGCAACATGTGTAAACAGGCAAAACGTGTTAAT	1179
QY	925	AAGAGGCCCTGCAGGCCAGCTGGCGCTGCTGTGGACCCACCGCCGCCCTGTTCGCC	984
Db	1180	AACAGAAATTACAGCAGAAGTTGGCTTGCGCTGTAGATCCAGACATTCCTGTTATAGTT	1239
QY	985	TTTCATCGCGCGCTGGAGGAGCAGAAGGTGTGGACATCATCTCTGGCGCGCTGCCCAAG	1044
Db	1240	TTTGTGGAGGCTGGAGGAGCAGAAGGTTTCAGATATTCCTAGCTGCAGCAATTCAGAA	1299
QY	1045	ATCCTGSCCAACCCCAAGGTGCAGATTCGCCATTCCTGGGTACCGGAGCGCCCTACGAG	1104
Db	1300	TTAATGSG--ATGAGAAGCTTCAGATCATATTCCTTGGAACTGGCAAGAAACACTCGAA	1356
QY	1105	AAGCTGTGNACGCCATCGGCCACAGTACAGGCGCGCCAGGGGGCTGTCAAGTTC	1164
Db	1357	AAGAGCTTGAAGAAATAGAAGACAATTTCCAGACACAGATGAGAGCTTGTTCGGAATTC	1416
QY	1165	TCGGCGCCCTGGCGCACATGCTCACCGCGCGCGCGACTTCATGCTGGTCCCTCGCGC	1224
Db	1417	AATGTTCCGTTGCTCATATGATGATGGCTGGAGGTATTTTATAATAATTCCTAGTAGA	1476
QY	1225	TTGAGCCCTGCGGCTGATCCAGCTGCAGCGCATCTAGCGGTACCGTCCGCGGTGGTA	1284
Db	1477	TTTGACCGCTGTGGGCTTATTGAGCTTGAAGGCATSAATATGGGATGCCAGCCATATGT	1536
QY	1285	GCTTCCACCGCGGCTGTGTCGACCGTCAAGGAGGCGCTCACCGGCTTCCACATGGCG	1344
Db	1537	TCACACACCGTGGTCTTGTAGACACATACAGGGAAGGCTTCCCGGATTTACATGGGT	1596
QY	1345	GCCCTGA-----ACCCGACAAAGCTGGACGAGGCTGACGCCGCGCGCTGGCGCCGAC	1398
Db	1597	GCCTTCACTGTTGAGTGTGAACCTGTGATCCGGTGGATGTGGCGGGAATTTGTTAAAAC	1656
QY	1399	GTGGCGGCTGCAGCAGGTGTTTGGGCGCGCGCTACCCCGAGATGGTGCCCACTGC	1458
Db	1657	GTAAGAGGGCCCTTAAGGTCTATGGAATCCAGGCTTTCAGCGAAATGGTTCAGAACTGC	1716
QY	1459	ATCAGCCAGCACTGCTCTGGTCCAAAGCCGCCCAAGTAGTGGGAGGGGCTGCTGCGAGAG	1518
Db	1717	ATGGCTCAAGATCACTCATGTGGAAGGACCTGCAAAAATAATGGAGAGACTACTCCTGGGA	1776
QY	1519	GTGGTGTACGGCAAGGGCG	1537
Db	1777	CTGGAAGCTCGACGGCAGCG	1795

```

RESULT 4
US-09-388-743-17
; Sequence 17, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Ian
; TITLE OF INVENTION: NO. 6423886el Starch Synthase Polynucleotides and Their
; TITLE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17

```

```
; LENGTH: 2274
; TYPE: DNA
; ORGANISM: Typha latifolia
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)...(1956)
US-09-388-743-17

Query Match      16.7%; Score 266.6; DB 4; Length 2274;
Best Local Similarity 52.9%; Pred. No. 2.5e-41;
Matches 828; Conservative 0; Mismatches 639; Indels 98; Gaps 8;

QY 1 GCGCTGACATCGTATGTTGCTGCTAGGTCGCGCCCTTGTCTCCAAAGACGGCGGCGCTG 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 GGGATGAACCTTACCTTTGTTGAGCTGAGATGCTCCATGGAGCAGAGCTGGAGGCGCT 432
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GGGATGAGCTGCTGGCTGCTGCTATGAGCTGGTCAAGCGCGCCACCGCGTCATGACC 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 433 GGTGATGTTCTTTGGAGGACTCCACCGCATTTGGCGCAATGGACATCGAGTTATGGTT 492
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 ATTGCCCTCGCTACACCACTAGCTGAGCGCTGGACCTCGGTGGTGGTGGACAT- 179
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 493 ATAGCCCAAGCTTATGATCAATACATGAGATGCTTTGGGATACAGATGCTCTTGTGATG 552
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 180 -----CATGGCGAGAGGTCCGCTACTTCCACTCCATCAAGAGGCGGTGCAC 228
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 553 AAGTTGGGATAGGTGTGAACCGTGGCTCTTTCATGCTATATAAGAGAGGTGAT 612
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 229 CGGGTGGATGACACACCCCTGGTTCCTGGCCAAAGTCTGGGGCAAGACCGGCTCCAAG 288
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 613 CGAGTTTGTGCTGATCACCTATGTTCTTGGGAAGTCTGGGGAAACTGTTGGGAAG 672
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 289 CTGTAGGCGCCCGCTCCCGGCTGACTACCTGGACACCAAGCGCTTGGCCCTGTTTC 348
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 673 ATTATGGTCTTAACACTGGAACAGACTATCAGGAATCAGTACGCTTCAGCTTCTCA 732
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 349 TGCAAGGCGCGCTATTGAGCTGCGCGCTGCTGCGCTTCGGCGCC----- 393
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 733 TGGCAGGAGCATTTGGAAGCTCTTAGAATCTTAATCTCAACACAGTAGTCTTCTCT 792
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 394 -----GGCGAGACGTGCTCTCTGTTGGCCACGACTGGCAGCTTCGCGCTTGTGCGCC 444
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 793 GGTCTTATGGGGAAGATGTTATCTTCTATTGCAATGATTTGACACACTTCTCTCTGCCA 852
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 445 GTCTCTGCTGAAGGACGAGTACAGCCCAAGGCGGCTGCTACCAAGGCGAAGTGGTGTG 504
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 853 TGTCTACTTAAGAGCATGTACCATCCCGTGGCATTTACAAAGACGCCAAGGTGTGCTTC 912
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 505 GCTATCCACACATCGCCTTCCAGGCGCCGCTGTTGGAGGAGGCTTTTCAAGGACAGGAAG 564
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 913 TGCATTACAAATATATACATACCAAGTCGATTTCTCCCTCAGACTTCGAATTTCTCAAT 972
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 565 CTGCCCCAGGCGCGCTTTGACAAGCTGGCGCTTCTCGGAGGCTATGCCAAGGTTTACACT 624
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 973 CTTCGCGAG-----AATTTCAATCT 993
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 625 GAGGCGACCCCATGAGGAGACGAGAGCCCGCTGACGGGAAAGACCTACAGAAG 584
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 994 TCTTTTCAGTTTCATGATGGGTACACAAAGCC-----TGTGAAGGAATGAAG 1041
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 695 ATCAACTGGCTGAAGGGTGGCATTTATCGCGCGCGACAAAGCTGGTACTGTGTCGCCCAAC 744
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1042 ATAAATTTGATCAAGCAGGAATCTTAGAATCAGACAGGCTTTTACAGTGGATCCATAT 1101
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 745 TACGCGACCGAGATCGTCCGATGCGCGCGGCTGTGGAGCTGGACCTGCATCCCG 804
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1102 TATGCACAGAGCTCTTTTCAAGAGAAGAAAGGGAGTGCAGTTGGACAACATTTTGGT 1161
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 805 GCGAAGGCGATTGAGGCGATTGTAACGCGCATGGACATGAGAGTGAACCCCAAGACC 864
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1162 GTGACCAAGTATCACAGGAATTTGTAATGGAATGTAATGATGGAATCCATTAA 1221
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 865 GACAAGTTCTCTGTCGCGCGCTTACGACCAAGAACAGCTTACGCGCGCAAGGCCCGCC 924
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 1222 GACAAGTATATTTCTGTATTAATTAATGATGCAAAACCTTAATGGAAGCAAAAGCCTTTAAAC 1281
QY 925 AAGGAGCCCTGCAGGCGG-AGCTGGGCGCTGCTGTGGAGCCACCCACCGCCCTGTTCGC 983
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1282 AAGGAACCATTTGAAGCTGAAGTTGGCTTGCCTGTAGACAGGAGACATCCCTGTAATGT 1341
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 984 CTTCAATCGCGCGCTGGAGGAGCAGAAAGGTTGGAGCATCATCTGCGCGCGCTGCCCAA 1043
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1342 ATTCAAT-GGAAGACTAGAGGAGCAGAAAGGATCATGATATTCTAGCAGCATCCATTCACGA 1400
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1044 GATCCTGGCCACCCCAAGCTGAGATGCGCATCTGGGTACCGGCAAGGCGCGCTACGA 1103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1401 GATCATGG----ATGAGAAATGTTCAAGCTAATTAATTTCTTGAACCTGGCAAGAAATGGA 1457
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1104 GAAGCTGGTGAACGCCCATCGGCACCAAGTACAAAGGCGCGCCCAAGGCGCTGGTCAAGTT 1163
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1458 GAATCAGCTTCAGAGTATGAGGAATGTTCCCGGACAAAGTGAGGCGAGTTATGAAGTT 1517
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1164 CTGCGCGCCCTGGGCGACAATGCTACCGCGCGCGGCGGACTTCAIGCTGGTGGCTCGCG 1223
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1518 CAATGCTCCCTTAGCTCACCAGATGACGGCGGAGCTGATATAATTGCTCATTCCAAGTCG 1577
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1224 CTTGCGCCCTGGGCGCTGATCCAGCTGACGCGCATGCTACGTTACCGTGGCGCTGGT 1283
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1578 ATTCGAACCAATCGGCGCTTATCCAGTTGCAAGGCATGCAATATGGAACGCTTCTGCGTG 1637
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1284 AGCTCCACCGCGGCTGTCGACACCGCTCAAGGAGGCGGTCACCGGCTTCCACATGGG 1343
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1638 TTCTCCACTGGTGGGCTTGTGGACAGGTGAAGAGGCAAACTGGATTCATATGGG 1697
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1344 CGCCCTCA-----ACCCCGACAAGCTGAGCGGCTGACCGCGACGCCCTTGGCGCGCAC 1397
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1698 ACCTTTCACTGCTGAATGCGAAGTGGTTCGATCTTCTGATGTAAGAAAGTTGTCACAAC 1757
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1398 CGTGGCGCGTGCAGCGAGTGTGTTGGGCGCGCGCTACCCCGAGATGTTGGCCAACTG 1457
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1758 TGTGAACCGCGCACTTAAGCTCATCGGCACACCTGCTTTGAGGATATGATCAAGAATTG 1817
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1458 CATCAGCAGGAGCTGCTCCTGTGTCACAGCCCGCCAGAGTGGAGGCGCTGCTGGAGGA 1517
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1818 CATGGCACAGAGCTCTCATGGAGGCGCTGCAAAAGACTGGAGCAAGTTCTACTGAA 1877
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1518 GGTGG 1522
   |||
Db 1878 CTGG 1882
```

RESULT 5

```
US-09-388-743-13
; Sequence 13, Application US/09388743
; Patent No. 6423886
; GENERAL INFORMATION:
; APPLICANT: Singletary, George
; APPLICANT: Zhou, Ian
; TITLE OF INVENTION: No. 6423886el Starch Synthase Polynucleotides and Their
; FILE OF INVENTION: Use in the Production of New Starches
; FILE REFERENCE: 1144
; CURRENT APPLICATION NUMBER: US/09/388,743
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2176
; TYPE: DNA
; ORGANISM: Canna edulis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81)...(1928)
US-09-388-743-13
```

Query Match 16.3%; Score 259.6; DB 4; Length 2176;
Best Local Similarity 51.6%; Pred. No. 5e-40;

QY 185 -----GCGAGAGGTCGCTACTTCACATCCATCAGAGGGCGTGCACCGG 232
DB 575 TTGGTGAATGAATGAATGTCGCTTTTCCACTGCTACAAAGGGAGTGATCGGG 634
QY 233 TGTGATGACCAACCCCTGTTCTGCGCAAGCTTGGGCAAGACCGGTCCAAAGCTGT 292
DB 635 TGTGTTGTGATCACCCTCTCTCTTGAGAGGTTTGGGAAAACCTGAGGAAATAT 694
QY 293 AGGCCCCCGCTGCGGCTGACTACTGACAAACACAAAGCGCTTGGCCCTTTCTGCA 352
DB 695 ATGGTCTCTCACAAGAACTGATATGAAGAACAAACAGCTAAGTTCTGTCTCTCTGTT 754
QY 353 AGGCGCTATTGAGGCTGCGCGCTGCTG-----CCCTTCGGCC 391
DB 755 TGGCACTCTGAAACTCCAAAGGTTCTGAATCCCAACAAATACAAATATCAATTCGAG 814
QY 392 CGGGGAGGACTGCGTCTTCTGCGCAACAGCTGGCACTCCGCCCTGTGGCGCTCTGC 451
DB 815 CAAAAGGTGAAGATTATTCATTGCTAAGCAATGGCACTGCTCTATTACCTTGTAAT 874
QY 452 TGAAGAC---CAGTACAGCCCAAGGGCCAGTTACCAAGGCCAAGTGGTCTGGCTA 508
DB 875 TAAAGACCAATTCATATCAAGCCCAATGGAATATACAAAATGCTAAAGTTGCTTTCTGCA 934
QY 509 TCCACAACATCCCTTCCAGGCGGCATCTGGGAGGAGCTTTCAGAGACACGAAGCTGC 568
DB 935 TWCATAATTCGGTATCAGGACGGTTTGGCCTTTGAAGATTTTTCGCGTCTCAATCTCC 994
QY 569 CCGAGCGCCCTTTGACAAGCTTGGCTCTCGACGGCTATGCAAGGTTTACACTGAGG 628
DB 995 CTGATACATCAAGTCTCTTTGATTTCATCGATGGCTATGCAAA-----1040
QY 629 CCACCCCATGAGGAGGACGAGAGCCCGCTGACGGGAAGACCTCAGAGAATCA 688
DB 1041 -----ACCAATAAAGGAAGGAATCA 1063
QY 689 ACTGGTGAAGGTTGCAATTCGCGCGCAAGCTGTGCTGCTGCGCCCACTAGC 748
DB 1064 ACTGATGAGCGGGAATATAGATCAGATCGTGCAATGACTGTGAGCCCATATATG 1123
QY 749 CAGCCAGATCTGCTCGGATCGCGCGGTGTGAGGCTGGACACCGTCTATCCCGCCA 808
DB 1124 CCGAGAACTCTCTCAGGAATCGATAGGGCGTGGAGTGGACATATACTCCGCTTA 1183
QY 809 AGGGCATTGAGGCGCATTTGACGGCATGGACATGAGAGTGGAAACCCCAAGACGACA 868
DB 1184 AAACCATCTGTGGCATCAFAAATGAATGGACACCAACAGTGGATCCCTCAACAGACA 1243
QY 869 AGTTCTCTGCTGCGCCCTACGACCAAGACAGGCTCTACCGCGCAAGCGCGCCCAAGG 928
DB 1244 TATCATACAGCAATACGACGCAACCACTGTATGAGGCAAGCCACTCAACAAG 1303
QY 929 AGGCCCCGAGCGGAGTGGGCTTGCCTGTGGACCCCAACCGCCCTGTCGCTTCA 988
DB 1304 AAGCTTTGCAAGCTGAGGTGGACTCGCGCTCAACAGTAAATCCCTGTGATAGTTTCA 1363
QY 989 TCGGCGCTGAGGACAGAGGTTGGACATCATCTCGCGCCCTGCCCCCAAGATCC 1048
DB 1364 TGGGCACTAGAAAGAAAAGGTTTCAGACATTTCTAGCTGAAGCAATTCAAAAGTTCT 1423
QY 1049 TGGCCACCCCAAGTGCAGATCGCCATCTCTGGTACCGCAAGCGCGCTACGAGAAGC 1108
DB 1424 T---CGATCAGATGTTCAAGTATAGTCTCGGTACTGGTAAAAGAGTTAGAGCGCC 1480
QY 1109 TGGTGAAGCCATCGGCACCAATACAAAGGCGCGGCAAGGCGGTGGTCAAGTCTCGG 1168
DB 1481 AACTTGTGATTCGAGGACGAGTTCCAGACAAATTCAGACCTCATATGAAGTTCAATA 1540
QY 1169 CGCCCTGGCGCATGCTCACCGCGCGGCGGCTGATGCTGCTGCTGCTGCTGCTGCTG 1228
DB 1541 TFCCTTTGGCTCATGGAATATGCGGGGTGCTGATATCTCTGTTATTCAGCTAGGTTG 1600
QY 1229 AGCCCTCGGCGCTGATCCAGCTGCGCAATGCACTACGCTACCGTGGCTGAGCT 1288

RESULT 7

US-09-196-390-5

; Sequence 5, Application US/09196390

; Patent No. 6307125

; GENERAL INFORMATION:

; APPLICANT: Block, Martina

; APPLICANT: Lorz, Horst

; APPLICANT: Lutticke, Stephanie

; APPLICANT: Walter, Lennart

; APPLICANT: Froberg, Claus

; APPLICANT: Kossmann, Jens

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES

; TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; FILING DATE: US/09/196,390

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 196 21 588.9

; FILING DATE: 29-MAY-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 196 36 917.7

; FILING DATE: 11-SEP-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP97/02793

; FILING DATE: 28-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Haley, Jr., James F.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: AGREVO-9

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 596-9000

; TELEFAX: (212) 596-9090

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2825 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

DB 1601 AACCATCGGCTCATTCAGTCCAGGCAATGATACGGAACCCCTTCCATGTGCACCA 1660
QY 1289 CCACCGCGGCGCTGGTGCACACCGTCAAGAGGCGGTCACCGGCTCCACATGGCGGCC- 1347
DB 1661 CGACTGGTGGCTGCTGCGACACTGTCAAGAAGGCATCACAGGTTTCCACATGGGTCCCT 1720
QY 1348 -----CTGACACCCCGACAAAGCTGGAGGCTGACGCGGACGCGCTGGCGCCACCGTGC 1402
DB 1721 TCAGTGGAGTGGACATTCGCCAGAGCGCGGCTTAAAGATGTGTGAAGCAGTGA 1780
QY 1403 GCGCTGCGACGAGGAGTGTGCGGCGGCGCGCTTACCCCGAGATGGTGGCCAACTGATCA 1462
DB 1781 AGAGAGCCCTTATGGTTTATGGAACGCTGCTTTCGAGGAGATGATACAGAAGTGCATGG 1840
QY 1463 GCCAGAGACCTGCTCTGCTCCAAAGCGCGCCAGAAAGTGGGAG 1503
DB 1841 CTCAGATTCTCTGGAAGGGGCCAGAAAGATGGGAG 1881

Db	1828	-----AGACCCGCGCATCGTCAACGGCATCGACAACATGGAGTGGAAACCCCGAGG	1878
Qy	833	GCATGAGCATTTAGAGAGTGGAAACCCAGACCGACAGTTCCTGTCGCGCCCTACAGCC	892
Db	1879	TGGACGCCACCTCAAGTCCGAGCGGTACACCAAGTTCTCCCTAGGACGC-----	1929
Qy	893	AGAACAGGCTTACGCCGCCAAGGGCGCGCCAAAGAGGGCCCTGCAGCGCAGCTGGGCC	952
Db	1930	-----TGGACTCCGCAAGCGGCAGTGCAGAGAGCCCTGCAGGCCAGCTGGGCC	1980
Qy	953	TGCTTGTGGACCCACCGCCCCCTTTTCGCTTCATCGCGCGCTTGGAGGACGAGAAGG	1012
Db	1981	TGCAGGTCCGCGCGACGTGCGCTGCTCGGCTTCATCGCGCGCTTGCAGCGGACAGAAG	2040
Qy	1013	GTGTGCATCATCTTGGCGCGCCCTGCCAAAGATCCTGGCCACCCGCCAAGTGCAGATCG	1072
Db	2041	CGGTGGAGATCATCGCGGAGCCATGCCCTGGATCGTG---AGCCAGAGCTGCGAGCTGG	2097
Qy	1073	CCATCTTGGGTACCGGCAAGGGCGGCTACGAGAACTGTTGAACGCCATCGGCACCAAGT	1132
Db	2098	TGATGCTGGCACCGGGCGCACAGACCTGGAGAGCATGTCAGACACTTCGAGCGGGAGC	2157
Qy	1133	ACAGGGCCGCGCCAAGGGCGTGGTCAAGTTCTCGGCGCCCTTGCSCGACATGCTCACCG	1192
Db	2158	ACCACGAAAGTTCGCGGGTGGTGGGGTTCTCGCTGCGCTTGGCGCACCGGATCACGG	2217
Qy	1193	CCGGCGCGACTTCATGCTGGTGGCCCTCGCGCTTCGAGCCCTTGGCGGCTGATCCAGTGC	1252
Db	2218	CGGGGGGACGGCGTCTCATGCCCTCCGCTTCGAGCCGTGGCGGCTGAACCACTCT	2277
Qy	1253	ACGCCATPGACTACGTACGTGCGCGTGGTAGCCTTCACCGGGGGGCTGGTCGACACCG	1312
Db	2278	ACGCCATGGCTACGGCACCGTCCCGCTGCTGCAGCGCTTCGCGGCGCTCAGGACACCG	2337
Qy	1313	TCAAGGAGGGCGTCAACGGCTTCACATGGGCGCTTGAACCCCGACAAAGTGGACAGG	1372
Db	2338	TGCGCGCTTCGACCCCTTCAACCACTTCGGGCTCGGTGGACGTTTCAGCCGCGCCGAGG	2397
Qy	1373	CTGACGCCGACGCCCTTGGCGGCCACCGTGGCGGTCACGAGAGGTGTTTCGGGCGCGCC	1432
Db	2398	CGCAACAGCTGATCGAGGGCGCTCGGGCACTGCTCCGACCTACCGAGACTTCAAGGAGA	2457
Qy	1433	GCTACCCCGAGATGGTGGCCAACTGCATCAGCCAGGACTGTCCTGGTCCAGGCCCGCC	1492
Db	2458	GCTGGAGGGCCCTCCAGGAGCGGGCATGTGCAAGACTTACGTCTGGGAGCACGCCGCCA	2517
Qy	1493	AGAACTGGGAGGGCCTGCTGGAGGAGGTGGTGTAC	1527
Db	2518	AGCTCTACGAGGAGCTCTCTGTTCAAGGCCCAAGTAC	2552

```

RESULT 8
US-08-941-445A-10
; Sequence 10, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; CURRENT APPLICATION DATA:

```


Db 2048 ARWSNTGGMGNCNTGYMGNMGNMGNATGCGNARGAYYTNHSNTGGGAYCAYGCMG 2107
QY 1490 CCCACAAGTGGAGGCGCTGCTGGAGGAGGTGGTGTAC--GGCAAGGGCGGGTGGCCAC 1547
Db 2108 CNGTNTATYAGGAYGCTNTGCTNAAGCNAARTAYCARTGGTTRGCGNAATYTRYNG 2167
QY 1548 GCGCAAGAAGGAGGAGATCAAGGTCCCGTGGCC 1581
Db 2168 CNACNMGNMGNMGNWSNTGYMGNMGNACNTGGAC 2201

RESULT 10
US-09-345-214-20
; Sequence 20, Application US/09345214
; Patent No. 6392120
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Broglie, Karen E.
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; TITLE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS
; FILE REFERENCE: BB-1147
; CURRENT APPLICATION NUMBER: US/09/345,214
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 060/094,436
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 2248
; TYPE: DNA
; ORGANISM: Zea mays
US-09-345-214-20

Query Match 13.0%; Score 207; DB 4; Length 2248;
Best Local Similarity 55.1%; Pred. No. 2.8e-30;
Matches 477; Conservative 0; Mismatches 370; Indels 18; Gaps 3;

QY 678 CAAGAAGATCAACTGGCTGAAGGGTGGCATTTATCGCCCGGCGGTGTGGAGCTGGACACCGT 737
Db 1331 CGACACGCCCAACATCTTTGCGCGGGTCTGAAGATGGCAGACCGGGTGTGACTGTGTC 1390

QY 738 GCCCAACTACCGACCGACGATCGCTGCCGATGCCGCGGCGGTGTGGAGCTGGACACCGT 797
Db 1391 CCGCGGTACCTGTGGAGCTGAACAGTGAAGCGCGCTGGCGCTCCAGACATCAT 1450

QY 798 C---ATCGCGCCCAAGGCATTTAGGGCATGTGAAGGCATGGACATTTGAGAGTGGAA 854
Db 1451 CCGTCTTAACGACTGGAAGATCAATGGCATGTGAAGGCATCGACACCGAGGTGGAA 1510

QY 855 CCCCAAGACCGCAAGTTCTCTGTGCGCCCTAGCAGCAGACACGCG-----T 902
Db 1511 CCCCAAGTGAAGTGAAGTTCCTGTGCGCGGTGCGAGCGGTACACCACTACTCCCTCGAGACAT 1570

QY 903 CTACGCGCGCAAGCCCGCCGCAAGAGGCGCTTCGAGCGCGAGCTGGCGCTGCCGTGTGGA 962
Db 1571 CGACGCTGGAAGCGGAGTGAAGCGGCGCTTCGAGCGGAGCTGGCGCTGGAGTGGC 1630

QY 963 CCCACCGCCCGCTGTTCGCTTATCGCGCCCTCGAGGAGCAGAGGCTGTGGACAT 1022
Db 1631 CGACGAGTGCCTGCTGCTGCGCTTCATCGGCGTCTGGATGGACAGAGGCGGTGGACAT 1690

QY 1023 CATCTTCGCGCCCTGCGCAGATCTGCGCCACCCCAAGTGCAGATCGGCATCTCTGG 1082
Db 1691 CATCGGAGACCGATGCGGTGATC---GCGGGGCGAGCGTGCAGCTGTGTGATCTGG 1747

QY 1083 TACGCGCAAGCCCGCTTACGAGAGTGTGTGAAGCCCTAGCGACCAAGTACAGAGCGCG 1142
Db 1748 CACGCGGCGCGCACTTGGACCAAGTGTGCACATCTTGAGCGGAGCATCCCAACAA 1807

QY 1143 CGCAAGGGGTGTCAAGTCTCGGCGCCCTCGGCACATGCTACCGCGCGCGCGCA 1202
Db 1808 GGTGCGGGGTGGGTGCGGTCTCGGTGCTTATGCGCATCATCGGCGCGCGCA 1867

QY 1203 CTTATGCTGGTGGCCCTCGCGCTTCGAGCCCTCGGCGCTGATCCAGCTGCAGCCCATGCA 1262
Db 1868 CGTGTGCTGATGCCCTCCGCTTCGAGCCCTCGGCGCTGAACCACTCTACGCGATGC 1927

QY 1263 CTACGCTACCGTGGCGGTGCTAGCTTCACCGCGCGCGCTGGCGACACCGTCAAGGAGG 1322
Db 1928 ATACGCGACCGTCCCTGTGTGTCACGCGCTGGCGCGCTCAGGGACACCGTGGCGCGT 1987

QY 1323 CGTCACCGGCTTCCACATGGCGCGCTGAACCCGCAAGCTGGAGAGGCTCACGCCGA 1382
Db 1988 CGACCGCTTCAGCGAGCGCGGCTCGGTGGACTTTTGACCGCGCGAGGCCAACAGCT 2047

QY 1383 CGCCCTGGCGCCACCGTTCGCGCTGCCAGCGAGTGTTCGCGCGCGCGCTTACCCCGA 1442
Db 2048 GATCAGCGCGCTCAGCACTGCTCGACACGTACCGGAACCTACGAGGAGCTGGAAGAG 2107

QY 1443 GATGCTGGCAACTGCATCAGCAGGACCTGCTCTGTGTCGAAGCCCGCGCGAGTGGGA 1502
Db 2108 TCTCAGGCGCGCGCATGTCGAGGACCTCAGCTGGGACCGCGGCTGAGCTCTACGA 2167

QY 1503 GGGCCTGCTGGAGAGGTGGTGTAC 1527
Db 2168 GGACGCTCTGTCAAGGCCAAGTAC 2192

RESULT 11

US-09-345-214-16/c
; Sequence 16, Application US/09345214
; Patent No. 6392120
; GENERAL INFORMATION:
; APPLICANT: Lightner, Jonathan E.
; APPLICANT: Broglie, Karen E.
; TITLE OF INVENTION: MODIFICATION OF STARCH BIOSYNTHETIC ENZYME GENE
; TITLE OF INVENTION: EXPRESSION TO PRODUCE STARCHES IN GRAIN CROPS
; FILE REFERENCE: BB-1147
; CURRENT APPLICATION NUMBER: US/09/345,214
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 060/094,436
; EARLIER FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Zea mays
US-09-345-214-16

Query Match 13.0%; Score 206.6; DB 4; Length 1798;
Best Local Similarity 55.0%; Pred. No. 3.3e-30;
Matches 476; Conservative 1; Mismatches 370; Indels 18; Gaps 3;

QY 678 CAAGAAGATCAACTGGCTGAAGGGTGGCATTTATCGCCCGGCAAGCTGGTGTGTC 737
Db 918 CGACACGCCCAACATCTTTGCGCGGGTCTGAAGATGGCAGACCGGGTGTGACTGTGAG 859

QY 738 GCCCAACTACCGACCGAGATCGCTGCCGATGCCGCGGCGGTGTGGAGCTGGACACCGT 797
Db 858 CCGCGCTTACCTGTGGAGCTGAAGACAGTGAAGCGCGCTGGGCGCTCCAGACATCAT 799

QY 798 C---ATCGCGCCCAAGGCATTTGAGGCGATGTGAACCGCATGGACATTTGAGGAGTGGAA 854
Db 798 CCGTCTTAACGACTGGAAGATCAATGGCATGTGAACGGCATTCGACACCGAGGTGGAA 739

QY 855 CCCCAAGACCGCAAGTTCTCTGTGCGCCCTAGCAGCAGACACGCG-----T 902
Db 738 CCCCAAGTGCAGTGCACCTGCGGTGCGAGCGGTACACCACTACTCCCTCGAGACAT 679

QY 903 CTACGCGCGCAAGCGCGCGCAAGGAGCGCTTCAGCGCGAGCTGGCGCTGCCGTGTGGA 962
Db 678 CGACGCTGGAAGCGGAGTGCAGAGCGCGCTTCGAGCGGAGCTGGCGCTGGAGTGGC 619

QY 963 CCCACCGCGCGCTGTGCTGCGCTTTCATGCGCGCGCTGGAGGAGCAGAGGTGTGGACAT 1022

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2007
US-08-941-445A-8

Query Match 10.1%; Score 161; DB 3; Length 2007;

Best Local Similarity 53.2%; Pred. No. 9.3e-22;

Matches 444; Conservative 0; Mismatches 370; Indels 21; Gaps 4;

QY 699 GGGTGGCATATCGCGCGGACAACTGGTACTGTGTGCGCCCACTAGCGACCGAGAT 758
DB 1170 GTGTGTTCTGAAGATGGACACCGCGGTGTGTACTGTGACGCGCGGTACTCTGGAGCT 1229
QY 759 CGCTCCGATGCCCGCGGTGTGGAGTGGACACCGTFC----ATCCGGGCCAAAGGGAT 815
DB 1230 GAAGACAGTGAAGCGCGGTGGGGCTCCACGACATCATCTCGTTCTAAGCACTGGAAGAT 1289
QY 816 TGAGGGCAATGTGAACCGCATGGACATTGAGGAGTGAACCCCAAGACCGGACAACTTCT 875
DB 1290 CAATGGCATTCGTGAACGATCGACACCGAGGAGTGAACCCCAAGTGGAGCTGCACCT 1349
QY 876 GTCTCGGCCCTAGACACCAAGACAGCG-----TCTACGCCGCAAGGCGCGCGC 923
DB 1350 GCGGTGCGACGGCTACACCAACTACTCCCTCGAGACACTCGACGCTGGAAGCGGCAGTG 1409
QY 924 CAAGGAGCCCTGAGCGCGGAGCTGGGCTGCTGTGACCCACCGCGCCCTGTTGCG 983
DB 1410 CAAGGCGCCCTGAGCGGGAGCTGGGCTGGAAGTGGCGGACGAGTGGCGCTGCTCGG 1469
QY 984 CTTATCGCGCCCTGAGGAGGAGAGAGGTTGTGACATCATCTCTGCGCGCCCTGCCCAA 1043
DB 1470 CTTATCGCGGCTGTGATGAGACAGAGCGCTGACATCATCGGGGACGAGTCCGTG 1529
QY 1044 GATCTGCGCACCCCAAGTGTGAGATCGCATCTCTGGGTACCGGCAAGCGCGCTACGA 1103
DB 1530 GATC---CGGGGAGGAGCGTGCAGCTGTTGATGTTGGGACCGGCCACCTGACCTGA 1586
QY 1104 GAAGCTGTGTAACGCCATTCGCGCACCAAGTACAGGGCGCGCCCAAGGGCTGGTCAAGTT 1163
DB 1587 ACGAATGTCGAGCATTTGGAGGCGGAGCATCCCAACAAAGTTCGCGGGTGGTGGGTT 1646
QY 1164 CTCGCGCCCTGCGGACATGCTCACCGCGGCGGAGTTCATGCTGTGCTGCTGCTGCGG 1223
DB 1647 CTCGCTCTATGTTGATCGATCATCACCGCGGCGGCGGAGCTGTGTTGATGTCCTCCG 1706
QY 1224 CTTGAGCCCTGCGGCTGTATCCAGCTGCACGCCATGACGTACGTAACGTCGCCGCTGGT 1283
DB 1707 CTTGCG---CGGGCGGCTGAACACAGCTCTACGCGATGCGCATACGCGACCGTCCCTGTG 1763

QY 1284 AGCTCCACCGCGCGCTGTGTCGACACCGCTCAAGAGGGGCGTCAACCGCTTCCACATGGG 1343
DB 1764 GCACGCGGTGGCGGCTCAGGAGCACCGGTGGCGCGCTTACCGCTTGGCGGACGCGG 1823
QY 1344 CGCCCTGACCCCGACAAAGCTGGACGAGGTGACGCGGAGCGCCCTGGCCGCCACCGTGG 1403
DB 1824 GTCGGGTGAGCTTTTGACGCGCGCGGAGGCGCAACAGCTGATGAGGTGCTGAGCCACTG 1883
QY 1404 CCGTGCAGCGAGGTGTTTTCGCGGCGCGCTACCCCGGAGATGGTGCCCAACTGCATCAG 1463
DB 1884 CCGTGCAGCGTACCGAACTACGAGGAGCTGGAAGAGTCTCCAGCGCGCGCATGTC 1943
QY 1464 CCAGGACCTGCTGCTGCTCAAGCCCGCCAGAAAGTGGAGGGCGCTGTGTCGAGGAG 1518
DB 1944 GCAGAACCTCAGCTGGGACCAACGCGCTGAGCTCTAGGAGGAGCTCTCTTCTCAAG 1998

RESULT 14

US-08-572-951-2

; Sequence 2, Application US/08572951

; Patent No. 5824790

; GENERAL INFORMATION:

; APPLICANT: KEELING, PETER L.

; APPLICANT: KNIGHT, MARY E.

; APPLICANT: GUAN, HANPING

; TITLE OF INVENTION: MODIFICATION OF STARCH

; TITLE OF INVENTION: SYNTHESIS IN PLANTS

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; ADDRESSEE: Intellectual Property Group of

; ADDRESSEE: Pillsbury Madison & Sutro LLP

; STREET: 1100 New York Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3918

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/572,951

; FILING DATE: 15-DEC-1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/346,602

; FILING DATE: 29-NOV-1994

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/263,921

; FILING DATE: 21-JUN-1994

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul N. Kokulis

; REGISTRATION NUMBER: 16,773

; REFERENCE/DOCKET NUMBER: 222957/1.02.15C

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 861-3000

; TELEFAX: (202) 822-0944

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2085 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-572-951-2

Query Match

Best Local Similarity

10.1%; Score 161; DB 1; Length 2085;

53.2%; Pred. No. 9.4e-22;

	Matches	444;	Conservative	0;	Mismatches	370;	Indels	21;	Gaps	4
QY	699	GGGTGGCATTATCCGCGCGACAAAGCTGGTGA	CTGTGCGCCAACTACGACCGAGAT	758						
Db	985	GTGTGTTCTGAAGATGSCAGACGGGTGGTGA	CTGTGCTCAGCGCGCTACCTGTGGGAGCT	1044						
QY	759	CGCTGCGGATCCGCGCGCGGTGTGGAGCTGG	ACACCGTC---ATCCGCGCCAGGGCAT	815						
Db	1045	GAAGACAGTGGAGCGCGCTGGGCGCTCCAG	CATCATCGTTCTAACGACTGGAAGAT	1104						
QY	816	TGAGGGCATTGTGAACGGCATGGACATTGAG	AGGTGGAACCCCAAGACCGACAAGTTCT	875						
Db	1105	CAATGGCATTCGTGAACGCTGACACCAAGAT	GTGNAACCCCAAGGTGGAGTGCACCT	1164						
QY	876	GTCTGCGCCCTAGACACAGAACAGCG-----	TTTACGCGCGCAAGCGCGCGCG	923						
Db	1165	CGGTGTGGAGGGCTTACACCACTACTCCCT	CGAGACACTCGACGCTGAAAGCGGCA	1224						
QY	924	CAMGAGGCGCTCAGCGCGAGCTGGCGCTGC	CTGTGTGACCCCAACCGCCCTCTTCGC	983						
Db	1225	CAMGCGGCGCTCAGCGGAGCTGGGCGCTGGA	AGTTCGCGAGACGCTGCCTCGG	1284						
QY	984	CTTCATCGCGCGCTGGAGGAGCAAGAGGTGT	GGACATCATCTCTGGCGCGCTCCGCAA	1043						
Db	1285	CTTCATCGGCGTCTGGATGGACAGAGGGGT	GGACATCATCGGGGACGGATCCCGTG	1344						
QY	1044	GATCCTGGCACACCCCAAGGTGAGATGCGCA	TCTTGGGTACCGCAAGCGCGCTACGA	1103						
Db	1345	GATC---GCGGGGAGGACGTGCAAGTGGT	GATGCTGGCGCACCTGACCTGGA	1401						
QY	1104	GAAGCTGGTGAAGCCCATCGCACCAAGTCA	AGGGCGCGCAAGGGCTGGTCAAGTT	1163						
Db	1402	ACGAATGCTGCAGCATTTGAGCGGGAGCAT	CCCAACAAGTGCAGCGGTGGTCCGGTT	1461						
QY	1164	CTCGGCGCCCTGGCGCACATGCTCACGCG	CGGGCCGACTTCATGCTGGTCCCTTCGG	1223						
Db	1462	CTCGGTCTTAATGTGATCGCATACCGCGG	CGCCACGCTGCTGTGTGATCCCTCCCG	1521						
QY	1224	CTTCAGCCCTCGCGCGGATGCTCAGCTGC	ACGCCCATACACTACGCTACCGCTCGT	1283						
Db	1522	CTTCTG---CGGCGGGCTGAACAGCTCTAC	CGATGGCATACGGCACCGTCCCTGTGT	1578						
QY	1284	AGCCTCCACCGCGCGCTGTGACACACCG	TCAAGAGGGCGCTCACCGGCTTCCATGG	1343						
Db	1579	GCACGCGTGGCGGGCTCAGGACACCGCT	GTGCGCGTTTCGGCGACGCCGG	1638						
QY	1344	CGCCCTGAACCCCGACAAAGCTGGAGAGCT	GAACCGCACGCCGCCACCGTGGG	1403						
Db	1639	GCTCGGTGTGACTTTTGACCGCGCGGAG	CGGCCAACAAAGCTGATCGAGGTGCT	1698						
QY	1404	CCGTGCCAAGCAGGTGTTTGGCGGCGCG	CTACCCGAGATGGTGGCAACTGCATCAG	1463						
Db	1699	CCTGCACAGTACCGAACTACGAGGAGAG	CTGGGAAGAGTCTCCAGGCGCGGATGTC	1758						
QY	1464	CCAGGACCTGCTCTGGTCCACCGCCG	CCGACGAAGTGGGAGGCGCTGCTGGAGAG	1518						
Db	1759	GCAGAACTCTACGCTGGGACACCGCGCT	GTAGCTCTACAGGACGCTCTTGTCAAG	1813						

REF: 15

```

RESOLUT 15
US-91-196-390-1
; Sequence 1, Application US/09196390
; Patent No. 6307125
; GENERAL INFORMATION:
; APPLICANT: Block, Martina
; APPLICANT: Lorz, Horst
; APPLICANT: Lutticke, Stephanie
; APPLICANT: Walter, Lennart
; APPLICANT: Froberg, Claus
; APPLICANT: Kossmann, Jens
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES
; TITLE OF INVENTION: FROM WHEAT WHICH ARE INVOLVED IN STARCH
; TITLE OF INVENTION: SYNTHESIS

```

NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/196,390
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 196 21 588.9
 FILING DATE: 29-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 196 36 917.7
 FILING DATE: 11-SEP-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP97/02793
 FILING DATE: 28-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley, Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: AGREVO-9
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2239 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Triticum aestivum L.
 STRAIN: cv. Florida
 HAPLOTYPE: ca. 21 d Caryopses
 IMMEDIATE SOURCE:
 LIBRARY: cDNA library in pBluescript sk (-)
 CLONE: pASSS
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..2017
 196-390-1

Query Match	7.4%	Score 118.2;	DB 4;	Length 2239;
Best Local Similarity	52.4%	Pred. NO. 8.1e-14;		
Matches 333; Conservative		0; Mismatches 293;	Indels 9;	Gaps 3;

Qy	686	TCAACTGGCTGAAGGGTGGCATATTGCGCGCCGACAAGCTGGTGACTCTGTGTGCGCCAACT	745
Db	823	TTAACTTTTGAAGAGGAGCAGTTGTGACAGCAGATCGGATTTGTACCGCTCAGTCAGCGGTT	882
Qy	746	ACGGAGCCAGATC---GCTGCCGATGCCCGCGCGGTGTGGAGCTGGACACCGCTCATCC	802
Db	883	ATTTCATGGGAGGTGCACAACCTGCTGAAGTGTGGACAGGGGCTCAATGAGCTCTTAAAGCTCCC	942
Qy	803	CGCCCAAGGSCATTGAGGCGCATTTGAACCGCATGGACATTCAGGAGTGGAAACCCCAAGA	862
Db	943	GAAAAAGTGTAATGATGAATGTAAATGGAAATTACATTAATGATTTGGAACCCCAACA	1002
Qy	863	CCGACAAGTTCCTGTCTGCGCCCTACGACCGACAACAGGCTCTACCGCGGACGAGCGCGCG	922
Db	1003	CAGCAAGTGTCTCCCTCATCATTAATCTGCGATGACTCT---CTGGAAGAGCCAAAT	1059

```
QY 923 CCAAGAGCCCTGAGCGCGAGCTGGGCGCTGCTGTGACCCACCAGCCGCCCTGTCG 982
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1060 GTAAAGCTGAATTGAGAGGAGTTGGGTTTACCTGTAAGGAGGATGTTCTCTCATTTG 1119
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 983 CCTTCATCGGCGCTGGAGGAGCAGAGGCTGTGACATCATCTGGCCGCCCTGCCA 1042
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1120 GCTTTATTGGAAGACTGATACCAAGAGGATGATCTCAATAAATGGCCATTCAG 1179
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1043 AGATCCTGGCCACCCCGAGGTGCAGATCGCATCTGTGGTACCGGCAAGCGCCCTAGG 1102
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1180 AGCTCATG---AGGGAGGACGTGCAATTGTCTATCTGGATCTGGGATCCAAATTTTG 1236
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1103 AGAAGCTGCTGAACGCCATCGCCACCAAGTACAAGGCCGCCCGAGGGCGTGGTCAAGT 1162
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1237 AAGGCTGGAAGAGATCTACCGAGTCGAGTTACAAGGATAAATTCGCTGGATGGTGGAT 1296
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1163 TCTCGCGCCCTGGCGCACATGCTCACCGCGCGCGGACATTCATGCTGGTGCCTCGC 1222
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1297 TTAGTGTTCAGTTTCCACAGAAATACTGCAGTTGCGATATATTGTAATGCCATCGA 1356
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1223 GCTTCGAGCCCTGGCGGCTGATCCAGCTGCACGCCATGCACTACGCTACCGTGCCTGG 1282
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1357 GATTTGAACCTTGCCTCTTAATCAGTATATGCTATGCAATATGTCAGTTCCCTGTA 1416
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1283 TAGCCTCGACCGCGGCGCTGGTTCGACACCGTCAAG 1317
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1417 TTCATGGAAGTGGGGGCGCTCCGAGACACAGTCGAG 1451
  || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: June 3, 2003, 15:32:10
Job time : 69.3196 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: June 6, 2003, 21:49:59 ; Search time 144.611 Seconds
(without alignments)
15416.986 Million cell updates/sec

Title: US-09-980-771A-8
Perfect score: 1593
Sequence: 1 gcgtgacatcgatggt.....ccgtgacgagagatcccc 1593

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	474.8	29.8	2267	9	US-09-961-077-25
2	314.6	19.7	2399	9	US-10-138-075-1
3	275.2	17.3	2179	9	US-10-138-075-3
4	218.2	13.7	2825	10	US-09-952-677-5
5	118.2	7.4	2239	10	US-09-952-677-1
6	94.2	5.9	790	10	US-09-966-881-44
7	83.2	5.2	1427	10	US-09-974-300-757
8	82.2	5.2	805	10	US-09-966-881-43
9	76.4	4.8	813	10	US-09-966-881-45
10	76	4.8	1318	9	US-09-934-900-15
11	74.4	4.7	2712	10	US-09-748-033-4
12	72.2	4.5	299	10	US-09-294-093B-3520
13	72.2	4.5	824	10	US-09-894-633A-83
14	70.8	4.4	1415	9	US-09-934-900-11
15	70	4.4	3624	9	US-09-988-462-6
16	69.6	4.4	1896	9	US-10-124-880-15
17	69.6	4.4	3468	9	US-09-988-462-2
18	68.2	4.3	2681	9	US-10-232-563-1
19	68	4.3	804	10	US-09-966-881-40

20	66.8	4.2	4810	9	US-10-138-221-6
21	66.6	4.2	826	10	US-09-966-881-41
22	65.2	4.1	1929	9	US-09-899-642-1
23	65.2	4.1	2109	10	US-09-815-242-7761
24	65.2	4.1	88421	9	US-09-976-059-1
25	63.6	4.0	1059	9	US-10-232-563-4
26	62.6	3.9	828	10	US-09-815-242-7971
27	62.6	3.9	13842	9	US-09-860-846-30
28	62.6	3.9	13842	9	US-09-988-384B-30
29	62.6	3.9	13842	9	US-09-836-821-30
30	62.6	3.9	13842	10	US-09-861-289-30
31	62.6	3.9	36778	9	US-09-860-846-5
32	62.6	3.9	36778	10	US-09-836-821-5
33	62.6	3.9	36778	10	US-09-861-289-5
34	62.6	3.9	37948	9	US-09-988-384B-5
35	62	3.9	660	10	US-09-815-242-7875
36	62	3.9	1185	10	US-09-887-576-784
37	61.4	3.9	2442	10	US-09-815-242-4030
38	61.4	3.9	15872	9	US-09-860-846-1
39	61.4	3.9	15872	9	US-09-988-384B-1
40	61.4	3.9	15872	9	US-09-836-821-1
41	61.4	3.9	15872	10	US-09-861-289-1
42	61.4	3.9	15952	9	US-10-171-311-51
43	61	3.8	5224	9	US-09-373-658-32
44	60.8	3.8	1248	9	US-09-860-846-7
45	60.8	3.8	1248	9	US-09-988-384B-7

ALIGNMENTS

RESULT 1

US-09-961-077-25
; Sequence 25, Application US/09961077
; Publication No. US20030014775A1

GENERAL INFORMATION:

APPLICANT: Zwick, Michael G.
Edlington, Brent E.
McSwiggen, James A.
Merlo, Patricia Ann Owens
Guo, Lining
Skokut, Thomas A.
Young, Scott A.
Folkerts, Otto
Merlo, Donald J.

TITLE OF INVENTION: COMPOSITION AND METHODS FOR MODULATION OF GENE EXPRESSION IN PLANTS

NUMBER OF SEQUENCES: 1263

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/961,077

FILING DATE: 21-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/679,645

FILING DATE: July 12, 1996

APPLICATION NUMBER: 60/001,135

FILING DATE: July 13, 1995

APPLICATION NUMBER: 08/300,726

Sequence 6, Appli
Sequence 41, Appli
Sequence 1, Appli
Sequence 7761, Ap
Sequence 1, Appli
Sequence 4, Appli
Sequence 7971, Ap
Sequence 30, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 7875, Ap
Sequence 784, App
Sequence 4030, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 51, Appli
Sequence 32, Appli
Sequence 7, Appli
Sequence 7, Appli

FILING DATE: September 2, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 219/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2267 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-961-077-25

Query Match 29.8%; Score 474.8; DB 9; Length 2267;
 Best Local Similarity 59.9%; Pred. No. 2.7e-105;
 Matches 978; Conservative 0; Mismatches 557; Indels 99; Gaps 7;

5 TGGACATCGTATGGTTCCTGCTGAGGTGCGCCCTTGGTCCAAAGACGGCGCCCTGGGCG 64
 418 TGAACGTCGCTTCGTCGGCGCCGAGATGGCGCGTGGAGCAAGACCGCGCCCTGGGCG 477
 65 ATGTGACTGGTGGCTGCTATTGAGTGTGTCAGAGCGCGCCACCGGCTCATGACCATG 124
 478 ACGTCCTGGGCGCTGCCCGCCGATGGCGCGAATGGGCACCGTGTATGGTCT 537
 125 CCCCTGCTAGACAGTACGCTGACGCTGGACACCTCGGCTGGTGTCTGACAT 179
 538 CTCCCGCTAGACAGTACAGGACGCTGGGACACCGAGCGTGTGCCGAGATCAAGA 597
 180 -----CATGGCGAGAGTTCGCTACTTCCACTCCATCAAGAAGSGCTGCACCGCG 232
 598 TGGAGACAGTACAGAGCTGAGTTCCTTCCACTGTACAGCGCGAGTGGACCGCG 657
 233 TGTGATGACCAACCCCTGTTCTGGCCAAAGGCTTGGGCAAGACCGGCTCCAAAGTGT 292
 658 TGTTCGTGACCAACCCCTGTTCTGGAGAGGTTTGGGAAAGACCGGAGAGATCT 717
 293 ACGGCGCGCTGCGGCGCTGACTACCTGGACACACCAAGGCTTCGCCCTGCTGCA 352
 718 ACGGCGCTGACGCTGGAACGAGTACAGGACCAACAGCTGCGGTACGCTATGCC 777
 353 AGCGCGCTATTGAGCTGCCCGCTGCTGCCCTTCGGC----- 390
 778 AGGACAGCTTGAAGCTCAAGATCTTGAGGCTCAACAACCACTTCTCCGGAC 837
 391 --CCGCGGAGGACTGCTTCTGTTGGCCAAAGCTGGCACTCGCCCTGTTGCCGTC 448
 838 CATACGGGAGGAGCTGCTGTTCTGCTGCAACAGCTGGCACACCGGCTCTCTGCTGT 897
 449 TGCTGAAGGACGAGTACAGCCCAAGGCGGCTTCAACCAAGGCGGCTGCTGGCTA 508
 898 ACCCTCAAGGAACTTACAGTCTCCACGCTCTACAGGACCAAGACCGCTTCTGCA 957
 509 TCCCAACATCGCTTCCAGGCGCCGATGTGGAGGAGGCTTCAAGGACACAGAGCTGC 568
 958 TCCACACATCTCTTACAGGCGCGTTCGCTTCTCCGACTACCGGAGCTGAACCTCC 1017
 569 CCCAGGCGCTTTGACAGTGGCTTCTCGGACGCTATGCCAAGGTTTACATGAGG 628
 1018 CGGAGAGATTCAAGTCGCTTCGATTTTCATCGACGGCTACGAGA----- 1064
 629 CCACCCCATGAGGAGGACGAGAGCCCGCTACGCGGAAGACCTACAGAAGATCA 688
 1065 -----CCGCTGGAAG-----GCCGGAAGATCA 1086
 689 ACTGGCTGAAGGCTGCAATTATCGCGCGCAAGCTGGTGTGCTGCTGCGCAACTAG 748
 1087 ACTGGATGAAGCGCGGATCTCTGAGGCGCGACAGGCTCTCACCGTTCAGCCCTACTACG 1146

749 CGACCGAGATCGCTGCCGATCCCGCGCGGTGGAGCTGGACACACCTCATCCGCGCA 808
 1147 CCGAGGAGCTCATCTCCGCGCATCGCAGGGCTCGAGCTCGACAACATCATGCGCTCA 1206
 809 AGGCATTGAGGCGATTGTGAACGCGATGGACATTGAGGAGTGGNACCCCAAGACCGCA 868
 1207 CCGGATCATCCGCGCATCGTCAACGCGATGAGCGTACGCGAGTGGACCCCAAGAGGACA 1266
 869 AGTTCTGCTGCGCCCTACGACCAAGAACGCTACGCGCGGCAAGCGCGCGCAAGG 928
 1267 AGTACATCGCTGAAATGACGCTGTCGACGCGCTGAGGCGCAAGCGCTGACACAGG 1326
 929 AGCCCTGACGCGGAGCTGGGCGCTGCTGTGGACCCCAACCGCCCTTTCGCTTCA 988
 1327 AGCGCTGACGCGGAGGCTCGGCTCCCGGTGGACCGGAACATCCGCTGGTGGGCTTCA 1386
 989 TCGCGCGCTGGAGGACGAGAAGGCTGTGGACATCATCTGCGCGCCCTGCCAAGATCC 1048
 1387 TCGGAGGCTGGAAGAGCAGAAAGGACCCCGAGCTCATGGGCGCCCAATCCCGAGCTCA 1446
 1049 TGGCACCCCAAG---GTGAGATCGCCATCTCTGGTACCGGCAAGCGCGCTACGAGA 1105
 1447 TGGACATGTTGAGGACGCTGCAGATCTCTCTGGCACCGGCAAGAAAGTTTCGAGC 1506
 1106 AGCTGTTGAACCCCATCGGACCAAGTACAGGCGCGCGCAAGGCGCTGGTCAAGTTCT 1165
 1507 GCATGCTCATGAGCGCGGAGGAGAGTTCCAGGCAAGGTGCGCGCCCTGGTCAAGTTCA 1566
 1166 CGGCGCCCTGGCGCACATGCTACCGCGCGCGGCTTCTATGCTGGCTCGCTCGCT 1225
 1567 ACGCGCGCTGGCGCACCATCATGCGCGCGCGGCTGCTGCTCGCGCTCACCGCGCT 1626
 1226 TCGAGCCCTGGGCGCTGATCCAGCTGCACGCTACCTACGTTACCGTGGCGCTGGTAG 1285
 1627 TCGAGCCCTGGGCGCTCATCCAGCTGCAGGCGCATCGATACGGAACGCGCTGCGCTGG 1686
 1286 COTCCACCGCGCGCTGGTTCGACACCGCTCAAGGAGGCGCTACCGGCTTCCACATGGCG 1345
 1687 GCTCCACCGGCTGAGCTGCTGACACCATCATCAAGGCAAGACCGGCTTCCACATGGGCG 1746
 1346 CCGTCA-----ACCGCGACAGCTGGAGGCTGAGCGCGCACGCTTGGCGCGCACCG 1399
 1747 GCCTCAGCTGCTGCTGCAACGCTGCTGAGCGCGCGGAGCTCAAGAGGTGGCCACCAT 1806
 1400 TCGCGCTGCCAGCAGGCTGTTGGGCGCGCGCTTACCCCGAGATGGTGGCGCACTGCA 1459
 1807 TCGAGCGCGCTCATCAAGGTGCTGCGCACGCGCGCTACGAGGAGATGTTGAGAACTGCA 1866
 1460 TCAGCCAGGACCTGCTGCTGCTCCAAAGCGCGCGCAAGGAGGAGGCTGCTGGAGGAG 1519
 1867 TGATCCAGGATCTCTCTGGAAGGCGCTTCCCAAGACTGGGAGAACGCTGCTGCTCAGCC 1926
 1520 TGGTGTACGGCAAGGCGCGCTGGCCACCGCCCAAGAGGAGGATCAAGGTCGCCCTG 1579
 1927 TCGGGTGC-----GCGCGAGCCAGGCGGTGCAAGGCGAGGAGATCGCGCGCTCGCA 1983
 1580 CCGAGAAGATCC 1593
 1984 AGGAGAACGTGGCC 1997

RESULT 2
 US-10-138-075-1
 ; Sequence 1, Application US/10138075
 ; Publication No. US20030087369A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Broglie, Karen E.
 ; APPLICANT: Butler, Karlene H.
 ; APPLICANT: Harvell, Leslie T.
 ; APPLICANT: Lightner, Jonathan E.
 ; APPLICANT: Orozco, Emil M.
 ; TITLE OF INVENTION: Granule-Bound Starch Synthase

:	FILE REFERENCE:	Bbl174 NA						
:	CURRENT APPLICATION NUMBER:	US/10/138_075						
:	CURRENT FILING DATE:	2002-05-02						
:	PRIOR APPLICATION NUMBER:	60/288,315						
:	PRIOR FILING DATE:	2001-05-03						
:	NUMBER OF SEQ ID NOS:	5						
:	SOFTWARE:	Microsoft Office 97						
:	SEQ ID NO 1							
:	LENGTH:	2399						
:	TYPE:	DNA						
:	ORGANISM:	Zea mays						
:	US-10-138-075-1							
	Query Match	19.7%;	Score 314.6;	DB 9;	Length 2399;			
	Best Local Similarity	53.6%;	Pred. No. 9.9e-67;					
	Matches 863;	Conservative 0;	Mismatches 649;	Indels 99;	Gaps 6;			
QY	1	GC	CTG	TAC	TGGATCGTGTGCTGTAGGTGTCGCCCTTGTTCCAGACGGCGGCGCCTG	60		
Db	503	GG	ATG	ACTATTGTATTGTGTGA	CACTGAACTGCAAGCATGGTGCAAACTGGTGCCCTC	562		
QY	61	GG	C	ATGTGACTGTGTGGCCCTGCCTATT	TGAGCTGGTCAAGCGCGCCACC	120		
Db	563	GG	T	ATGTTTAGAGGAGCTGCCCCCAGCTTT	TGCTGCTATGGGACACCGTGTCA	622		
QY	121	ATT	GC	CCCCCTCGCTACGACAGTAGT	AGCTGACGCCTGGCACACCTCGTGGTGGTGAGCAT-	179		
Db	623	AT	A	GTCTCTCGTTAATGATCAATA	CAAGGATGCATGGGATACAAGTGTCTTTGTTGAGTA	682		
QY	180	-	-	-	-	-		
Db	683	AAT	ATT	GGTGACACGGTAGAACTGT	TCGCTCTCTCCACTGCTACAAAAGAGGATGAT	742		
QY	229	CG	CGT	TGGATTGACACACCCCTG	TTCCTGGCCAAGTCTGGGCAAGACCGGCTCCAAG	288		
Db	743	CG	T	TTTTTTTGATCATCTATGTTTCT	TGAAAAAGTATGGGCAAGACTGGAGCAAAA	802		
QY	289	CT	G	TAGGGCCCCGCTCCGGCGT	GACTACTGGACACCAACACAGCGCTTCGCGCTGTC	348		
Db	803	TGT	AT	TGGTCTACTTGGAACT	GTACTGAGATAACCAAGTTGAGGTTCTGCCTTTG	862		
QY	349	TGC	AAG	CGCCCTATTGAGGCT	GGCCGGTCTGCGCTTGGC-----	390		
Db	863	TGC	CTT	GTGCTTTGGAGGCT	CCCAAGAGTTCTCAATTCAACRAATCTGAATTTCTCT	922		
QY	391	-	-	-	-	-		
Db	923	GG	ACC	ATATGGGGAAGATGTGTCT	CGTAGCCAATGATTGGCACACTGCTATTTTGCCA	982		
QY	445	GT	C	CTGCTGAAGACAGTACCA	CGCCCAAGGGCCAGTTCACCAAGGCCAAGTCGGTCTG	504		
Db	983	TGT	AT	TCTGAGAGCATGTATA	AGCCAAATGGAAATTTATAAAATGCTAAGGTTGCTTC	1042		
QY	505	G	T	ATCCACAACATCGCCT	TCCAGGCCGCGATGTGGAGGAGGCTTTCAAAGGACACCAAG	564		
Db	1043	TGC	A	TACATAAATATGCTAT	CAAGTAGATTTGCCAGACAGACTTCGATCTCTTAAT	1102		
QY	565	CT	C	CCCCCGCCCTTTGN	CAAGCTGGCCCTTCGGAACGGCTATGCCAAGTTTACACT	624		
Db	1103	CT	A	CTGACAGTTTCTTG	CCATCATTTATTGATGGACATGTAAAGCCTGTTCTA	1162		
QY	625	G	A	G	G	G		
Db	1163	GG	-	-	-	-		
QY	685	AT	C	A	CTGCTGAAGGGTGGCA	TATTCGCCCGCAGCAAGCTGGTGTGTCGCGCCAAC	744	
Db	1172	CT	T	A	CTGATGAAGCAGGGAT	CATTGAGAGTGATCTGTTCTAACAGTCAGTCACAT	1231	
QY	745	T	A	G	C	G		
Db	1232	T	A	T	G	T		

; TYPE: DNA
; ORGANISM: Glycine max
US-10-138-075-3

Query Match 17.3%; Score 275.2; DB 9; Length 2179;
Best local similarity 52.7%; Pred. No. 3e-57;
Matches 820; Conservative 0; Mismatches 628; Indels 108; Gaps 6;

QY 11 TCGTGATGTTGCTGAGTGCCTCCCTTGGTCCAGAGCGGGCGGCGGCGATGGA 70
DB 323 TCATAATATAGGAACCGAGGTGCTCCATGGTCAAAACCTTGGTGGGATGTC 382
QY 71 CTGTGGCCTGCTATTGAGCTGGTCAAGCGCGCCACCGCTCATGACCATTCGCCCTC 130
DB 383 TTGAGGCTACCAACCGCATGCGAGTTTGGGCATCGAGTAATGACATTGCGCGC 442
QY 131 GCTACGACGATGAGCTGACGCTCGGACACCTCGGTGGTGGTGGACATCATG-- 184
DB 443 GCTATGACCATGACAAAGATGATGGATGATCAAGTGTGTAATGAGGTGAAGTAGGAG 502
QY 185 -----GCGAGAGGTCGCTACTTCCACTCCATCAAGAGGGCGTGCACCGCTGGGA 238
DB 503 ATAGAACAGAAAGTTGCTCTTCCATGTTATAGAGGGGAGTTGATGCTGTCTTG 562
QY 239 TTGACACCCCTGCTTCTGCGCAAGGTCTGGGCAAGACCGGCTCCAAGCTGTACGGCC 298
DB 563 TGGATCACCCCTTGTCTTGAAGAGTATGGGGAAACCTGGACAAAACCTTTATGGAC 622
QY 299 CCGCTCGGGGCTGACTACCTGGACACACACAGCGGTTCGCCCTGTCTGCAAGGCG 358
DB 623 CAACTACTGGAATGATACGAAGACACCAACTGCGTTTAGCCTTTTGGCAGGCTG 682
QY 359 CTATTGAGGCTGCGCGGTGCTGCCCTTCGCGCCC-----G 394
DB 683 CTTTGGAGCCCAAGGTTCTGAGTCTTATTCAGTAATATTTCTCTGGACCAATG 742
QY 395 GCGAGGACTCGCTTCTGCGCAAGCTGCGACTCGCGCTCGCGCTGCGCGCTGCTGTA 454
DB 743 GTGAAGATGTCATTTTGTCCCAATGATGGCACACTGCGCTTATCCCTGCTACTTGA 802
QY 455 AGGAGGATGACGCCCAAGGCGAGTTCACCAAGGCAAGCTGCTGCTGCTATCCACA 514
DB 803 AAGTATGTACAGTCAAGGGGCACTATACGAATGCCGGGTGTTTTTGTATCCACA 862
QY 515 ACATCGCCTTCCAGGCGCGATGTGGGAGGAGGTTTCAAGGACACGAGTGCCTCCAGG 574
DB 863 ACATGCTTACCAAGGAATGTCATTCGCGGACTTCTCACTTAAATCTCCAGACC 922
QY 575 CCGCTTTGACAAGCTGCGCTTCTGCGAGGCTATGCCAAGTTTACACTGAGGCCACCC 634
DB 923 AATTAAGAGCTCTTTCACCTTATTTGATGGCATG-----958
QY 635 CCATGGAGGAGGACGAGAAGCCCGCTGACGGGAAGACCTACAAAGATCAACTGGC 694
DB 959 -----TTAACCAGTGGTGGAGGAAATCAATGGT 991
QY 695 TGAAGGTGGCATTATCCCGCGCAAGCTGGTGAAGTGTGCGCCCAACTACGCGACCG 754
DB 992 TGAAGCTGGACTTATGAATCATGTTTGTGATAACCGTTAGTCCAACTATGCTAAAG 1051
QY 755 AGATCGCTGCGATGCCCGCGGCTGAGCTGGACACCGCTCATCGCGCCCAAG-- 811
DB 1052 AACTGGTGTGCTGAGTCCAGACAAAGAGGTGGAATTTGCAACATCATTCGCAAAATGTATG 1111
QY 812 -----GCATTGAGGCAATTGGAACGGCATGAGCATTCAGAGTGGAAACCCCAAGA 862
DB 1112 ATGATGTCGTTTGGTGGATTTGGAATGCAATGCAATGCTTCAGAGTGGATCAACCA 1171
QY 863 CGCAAGTTCCTGCTGCGCCCTACGACCAAGACAGCTGTACCGCGCAAGCGCGCG 922
DB 1172 CTGCAAAATATATAGCTGCAAAATATGATTTTCAACAGTATTTGAAGCAAGGCTCTTC 1231
QY 923 CCAAGGAGGCGCTGACGCGGAGCTGGCGCTGCTGCGACCCCAAGGCGGCTGCTG 982

DB 1232 TGAAGAAGCCCTCCAGCAGAAGTTGGATTGCCAGTGCACAGAAATATTCCTCTCATG 1291
QY 983 CTTTCATCGCGCGCTGAGGAGCAGAAGGTTGGACATCATCTGCGCGCTGCCCA 1042
DB 1292 GTTTCATTGGTAGGCTTTGAAGAGCAAAAGGTTCTGATATCTTGCAGAGCAATCCCC 1351
QY 1043 AGATCCTGGCCACCCCAAGGTGCAGATCGGCATCCTGGGTACCGCGCAAGCGCCTACG 1102
DB 1352 AATTAT---CAAGCAGATGTTCAAGTTGGTAGCCTAGGAACAGAAAAACAATGG 1408
QY 1103 AGAAGCTGGTGAAGCCCATCGGCACCAAGTACAGAGCGCGCCCAAGGCGGTGGTCAAGT 1162
DB 1409 AAAAGCAGCTTGAGGAACCTTGAATATATCATACCTGTATAGGCCAGAGAGTGGCAAAAT 1468
QY 1163 TCTCGCGCCCTGCGCACATGCTCACCGCGCGCGGCTTTCATGCTGTGCGCCTCGC 1222
DB 1469 TCAATGTTCCCTAGCCACATGATAATAGCTGGAGCTGATTTATATGTTGTTCTACGA 1528
QY 1223 GCTTCGAGCCCTGCGGCTGATCCAGCTGCAGCGCATCAGTACGTTACCGCTGCGCGTGG 1282
DB 1529 GATTGAGCCCTTGTGCTCATTCAGTTACAGCTATCGCTATGATCTGTACCAATG 1588
QY 1283 TAGCCTCACCGCGCGCTGCTGACACCGTCAAGAGGCGGTACCGGCTTCCACATGG 1342
DB 1589 TTGCTCAACAGGTGATTTAGTGTACACTGTCAAGAGAGGCTTCACTGGATTTCAGATGG 1648
QY 1343 GCGCCTCGA-----ACCCCGACAAGCTGGAGGCTGACCGCGCGGCTTGGCGCGCA 1396
DB 1649 GTGCTTCAATGTTGAATGATGCTGTGGATCCGCTGATGATGCTATATCAAGA 1708
QY 1397 CCGTGGCGCGTCCAGCGAGGTGTTTGGCGGCGGCGCTACCGCGAGATGGTGGCGCACT 1456
DB 1709 CTGTCAAAAGGCGCCTTGCAGTCTATGGAACITCCAGCTTTTACAGAAATTTATCAAGA 1768
QY 1457 GCATCAGCAGGACCTGCTTCCTGTCACAGCCCGCCAGAGTGGAGGCGCTGCTG 1512
DB 1769 GCATGGCTCAAGATCTTTCATGGAAGGCGGCTGCTAAGAGTGGGAGGAGTGGCTG 1824

RESULT 4

US-09-952-677-5

; Sequence 5, Application US/09952677

; Patent No. US20020138876A1

; GENERAL INFORMATION:

; APPLICANT: Block, Martina

; Lorz, Horst

; Lutticke, Stephanie

; Walter, Lennart

; Frohberg, Claus

; Kossmann, Jens

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES

; FROM WHEAT WHICH ARE INVOLVED IN STARCH

; SYNTHESIS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: United States of America

; ZIP: 10020

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA: US/09/952,677

; FILING DATE: 14-Sep-2001

; PRIOR APPLICATION NUMBER: 09/196,390

; APPLICATION NUMBER: 09/196,390

; FILING DATE: 19-No. US20020138876A1-1998

Query Match	13.7%	Score 218.2	DB 10	Length 2825	
Best Local Similarity	50.1%	Pred. No. 1.6e-43			
Matches 769	Conservative	0	Mismatches 688	Indels 78	Gaps 6
QY	5	TGGACATCGTGATGGCTTGCTGCTGAGTGCCTCCCTTGGTCCACAGACGGGCGGCTGGGCG	64		
Db					
1084	TGAACGTGGTCTGCGTGGCTGCTGAGTGTCTCCTCGTGCACAAACAGGTGGTCTGGGAG	1143			
QY	65	ATGTGACTGGTGCCTTGCCTATTGAGCTGCTCAAGCGCGCCACCGCGTCAATGACCAATTG	124		
Db					
1144	ATGTTGGGGTGTCTGCCCCAAGCTTTGCCAAGAGAGACATCGTGTTATGGTTGTGG	1203			
QY	125	CCCTCGCTACGACCACTAGCTGAGCGCTGGACACCTCGGTGGTCTGGACATCATGG	184		
Db					
1204	TACCAAGGTATGGGACTATGAAGAAGCCTACCATGTCGGAGTCCGAAATATACAAAG	1263			
QY	185	GCGAAGGTCCGCTACTTCCACTCCATCAAGAAGCGGCTGCACCGCGTGTGGATTGACC	244		
Db					
1264	CTG-----CTGGACAGGATATGGAAGTGAATTATTCATCTTATATCGA	1309			
QY	245	ACCCCTGGTTCCTGGCCAAAGTCTGGGGCAAGACCGGCTCCAAGCTGTACGGCCCGCGCT	304		
Db					
1310	TGGAGTGAATTTGTGTTGCTCATGACGCTCCTCTCTTCCGAC-ACCGTCAGGAAGACATTT	1368			
QY	305	CGGGCGCTGACTACCTTGGACAAACCAAGCGCTCGCCCTGTCTCAAGCGCGCTATTG	364		
Db					
1369	ATGGGGCAGCAGACAGGAATATCAAGCGCATGATTTGTTCTCAAGCGCGCTGTTG	1428			
QY	365	AGGCTCCGCGTGTGTCCTCTGGCCCGGCGGAGGACTCGG-----TCTTCG	412		
Db					
1429	AGGTTCCATGGCAGGTTCCATGGGCGGTGTCCTTATGGGATGGAATCTGGTGTTTA	1488			
QY	413	TGCCAACGACTGGCACTCGGCCCTGGTCCGCCCTCTGCTGAAGCAGGAGTACCAACGCCA	472		
Db					
1489	TTGCAATGATTTGGCACAGGCACTCCTGCCCTGCTATCTGGAAGCATATTACAGGGACC	1548			
QY	473	AGGGCCAGTTTACCAGGGCCAGTCCGTGCTGTATVCCACAACATCGCCTTCCAGGGCC	532		
Db					

QY	746	ACGCCACCGAGATC---GCTCCGATGCCGCCGGGGTGGTGGAGCTGGACACCGCTATCC	802
Db	883	ATTCAATGGGAGGTACAAACTGCTGAAGGTGGACAGGGCTCTAAATGAGCTCTTAAGCTCCC	942
QY	803	CGGCCAAGGCAATTGAGGCAATTGTGAACGGCATGGACATTTGAGGAGTGAACCCCAAGA	862
Db	943	GAATAAGGTATTGAATGGAATTGTAATGAATTTGACATTAATGATTTGAATGGAACCCCA	1002
QY	853	CCGACAAGTCTCTGCTCGCCCTACGACAGACAGAGCTCTACCCGCGAAGCCGCGG	922
Db	1003	CAGACAAGTGTCTCCCTCATATTATTCTGCGATGACCTCT---CTGGAAGGCGCAAT	1059
QY	923	CAAGGAGGCGCTGCAGCGCGAGCTGGCGCTGCGCTGTGGAGACCCACCGCCCGCTGTTCG	982
Db	1060	GTAAGCTGAATTGCAGAGGAGTTGGGTTTACCTGTGAAGGAGGATGTTCTCTGATTG	1119
QY	983	CTTCATCGGCGCTGGAGGAGCAGAAGGGTGTGGACATCATCTCGGCGCCGCTGCGCA	1042
Db	1120	GCTTTATTGGAAGACTGGATTACCAGAAAGCAATTGATCTCATTTAAATGGCCATTCAG	1179
QY	1043	AGATCTGCGCACCCCAAGGTGCAGATCGCATCTGGTACCGGCAAGCGCGCTACG	1102
Db	1180	AGCTCATG---AGGAGGACGCGCAATTGTCATCTGTGATCTGGGATCCAAATTTG	1236
QY	1103	AGAAGCTGTGAACGCCATTCGGCACCAAGTACAAAGGGCGCGCCCAAGGGCGTGTCAAGT	1162
Db	1237	GAAGCTGGATGAGATCTACCGAGTCGAGTTACAAGATAAATTCGGTGGATGGTTGGAT	1296
QY	1163	TCCTGCGCGCTGCGGCACATGCTCACCGCGCGCGGACATTCATGCTGGTGGCGCTCG	1222
Db	1297	TTAGTGTTCACAGTTTCCACAGAAATCACTGCAAGTTGCGATATATTGTTAATGCCATCGA	1356
QY	1223	GCTTCGAGCGCTGCGCGCTGATCCAGCTGCAGCGCATCACTACGTTACCGTCCCGCTGG	1282
Db	1357	GATTTGAACCTTGCCTTAAATCAGCTATATGCTATGCAATATGCTACAGTTCTCTGTAG	1416
QY	1283	TAGCTTCCACCGCGCGCTGGTTCGACACCGCTCAAG	1317
Db	1417	TTCAATGGAACCTGGGCGCTCCGAGACACAGCTCGAG	1451
RESULT 6			
US-09-966-881-44			
; Sequence 44, Application US/09966881			
; Patent No. US20020120960A1			
; GENERAL INFORMATION:			
; APPLICANT: Seymour, Graham			
; Bird, Colin			
; Medina-Suarez, Rosybel			
; TITLE OF INVENTION: Genetic control of Fruit Ripening			
; NUMBER OF SEQUENCES: 57			
; CORRESPONDENCE ADDRESS:			
; ADDRESSER: Zeneca Ag Products Inc.			
; STREET: 1800 Concord Pike			
; CITY: Wilmington			
; STATE: DE			
; COUNTRY: USA			
; ZIP: 19850			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/966,881			
; FILING DATE: 28-Sep-2001			
; CLASSIFICATION: <Unknown>			
; PRIORITY APPLICATION DATA:			
; APPLICATION NUMBER: US/09/242,850			
; FILING DATE: 29-Mar-1999			
; APPLICATION NUMBER: GB 9618862.3			
; FILING DATE: 10-SEP-1996			

Sequence 1, Application US/09952677

Patent No. US20020138876A1

GENERAL INFORMATION:

APPLICANT: Block, Martina

Lorz, Horst

Lutticke, Stephanie

Walter, Lennart

Frohberg, Claus

Kossmann, Jens

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ENZYMES FROM WHEAT WHICH ARE INVOLVED IN STARCH SYNTHESIS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,677

FILING DATE: 14-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/196,390

FILING DATE: 19-NOV-2002

APPLICATION NUMBER: DE 196 21 588.9

FILING DATE: 29-MAY-1996

APPLICATION NUMBER: DE 196 36 917.7

FILING DATE: 11-SEP-1996

APPLICATION NUMBER: PCT/EP97/02793

FILING DATE: 28-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Haley, Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: AGREVO-9

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2239 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Triticum aestivum L.

STRAIN: cv. Florida

HAPLOTYPE: ca. 21 d Caryopses

IMMEDIATE SOURCE:

LIBRARY: cDNA library in pBluescript sk (-)

CLONE: TsSS

FEATURE:

NAME/KEY: CDS

LOCATION: 3..2017

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-952-677-1

Query Match 7.4%; Score 118.2; DB 10; Length 2239;

Best Local Similarity 52.4%; Pred. No. 1.9e-19;

Matches 333; Conservative 0; Mismatches 293; Indels 9; Gaps 3;

QY 686 TCAACTGGCTGAAGGTGG

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,881
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/242,860
FILING DATE: 29-Mar-1999
APPLICATION NUMBER: GB 9618862.8
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: GB 9708366.1
FILING DATE: 25-APR-1997
APPLICATION NUMBER: PCT/GB97/02424
FILING DATE: 08-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: SEE 50183/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: U-D66
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-966-881-43

Query Match 5.2%; Score 82.2; DB 10; Length 805;

Best Local Similarity 57.8%; Pred. No. 8.8e-11;

Matches 170; Conservative 0; Mismatches 111; Indels 13; Gaps 1;

QY 1 CGCTGGACATCGTGTGCTGAGTCGCCCTTGTCTCAAGACGGGGCGCTG 60
DB 310 GGGATGACATAGTCTTTGTGCGGCTGAGATGGCTCCTGGANTAAACCGGAGACTC 369
QY 61 GCGGATGACTGTGGCTCCCTATGAGCTGTGTCACGCGGCCACCGGTCATGACC 120
DB 370 GGTGATGTCTTGAGGAGTCCACCGGCCATGGCTGCAATGGACACACAGTGATGACT 429
QY 121 ATTGCCCTCGCTAGCAGCAGTACGCTGACGCTGGGACACCTCGGTGTCG----- 172
DB 430 ATAGCTCCACGCTATGATCAGTACAAGGATGGTGGGATACAAATGTCTCGCTGANTTA 489
QY 173 -----TGGACATCATGGCGGAGAGGTCCTGCTACTTCCATCCATCAAGAAGGGGTGCA 227
DB 490 AAANTTGAATGAATTTGAAGANTCCGCTCTTCCACTGCTATAAANAGATTCA 549
QY 228 CCGCGTGTGATGATACACCCCTGTTCTGCGCCAAAGTCTGGGCAAGACCGG 281
DB 550 CAGGTTTTCATGATCATCTTTGTTTCTTGAAAAAGTGTGGGAAAAACTGG 603

RESULT 9

US-09-966-881-45/c

; Sequence 45, Application US/09966881

; Patent No. US20020120960A1

; GENERAL INFORMATION:

; APPLICANT: Seymour, Graham

; Bird, Colin

; Medina-Suarez, Rosybel

; TITLE OF INVENTION: Genetic control of Fruit Ripening

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zeneca Ag products Inc.

; STREET: 1800 Concord Pike

CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,881
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/242,860
FILING DATE: 29-Mar-1999
APPLICATION NUMBER: GB 9618862.8
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: GB 9708366.1
FILING DATE: 25-APR-1997
APPLICATION NUMBER: PCT/GB97/02424
FILING DATE: 08-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: SEE 50183/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: U-D112
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-966-881-45

Query Match 4.8%; Score 76.4; DB 10; Length 813;

Best Local Similarity 54.8%; Pred. No. 2.2e-09;

Matches 194; Conservative 0; Mismatches 153; Indels 7; Gaps 2;

QY 1157 TCAAGTTCTGGCGCCCTCGGCACATGCTCACCGCGCGCCGACACTCATCGTGGTGC 1216
DB 535 TGAAGTTTAATGCACCTTTGGTGCATGAAATCATGGCTGGAGCACTTCTTGTCTTTA 476
QY 1217 CCTCGGCTTCAGCCCTCGCGCCATCCAGC-TGCAGCCCATGCACCTACCGTACCGTG 1275
DB 475 CCAGCAGATTGCAACCTTTGGCCCTATCCAGCTTTCAGGGCATCGGATATGGAATCCC 416
QY 1276 CCGCTGGTAGCCTCCACCGCGCCCTGGTGCACACCGTCAAGGAGGGCGTCAACCGGCTTC 1335
DB 415 CCCATGTGCGCAACAACTGGTGGACTGCTGACACTGTCTAAGAGGCATCACAGGTTT 356
QY 1336 CACATGGGCGCCCTGAACCCCGACAAAGCTGGAGGCTGACCGCGACGCCCTGGCCGCC 1395
DB 355 CATATGGTCCCTTCAATCCTGATTGTGATGTGTGATATAAGATGATGTACAAAAGTC 296
QY 1396 -----ACGCTGGCGGCTCCAGCGAGGTGTTTGGGGGGCGGCTACCCCGAGTGGTG 1449
DB 295 ATTCAGACAGTGAAGAGGGCCCTTAAAGTTTACGGCACACCTGCAATTCCTGAGATGATA 236
QY 1450 GCGAACTGCATCAGCAGGACCTGCTGCTCCAGCGCCCGCCGAGAGTGGAG 1503
DB 235 CAGAACTGCATGACTCAAGACCTCTCTTGAAAGGACCTGCTAAGAAAGTGGAG 182

RESULT 10

US-09-934-900-15

; Sequence 15, Application US/09934900

; Publication No. US20030054521A1

Db 1455 CGGTCCAGGCGCGACACACCGCGACAGACCGCGCGGTACGCGCCCGCGTCAAGGTCA 1514
QY 1166 CGGCGCCCTGGGCGACATCTACCGCGCGCGCGGCGGACTCATCTGTTGCCCTCGCGCT 1225
Db 1515 CCACCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1568
QY 1226 TCAGCGCTGCGGCGCTGATCCAGCTGACGCTGACGCGCATCTAGCTAGCGTACGCGCGGTAG 1285
Db 1569 TCGCTACTTACCGAGTGGGCGGTCTACGCGCGCACTACCACTGCAAAACCTGGTGA 1628
QY 1286 CTTCCACGGGCGGCTGCTGACACCTGCTAAGAGGCGGTACCGGCTTCCATATGGGCG 1345
Db 1629 CTTCCGCGTCCGCGGAGAGTACCCACCTACTCTCTCGGCAACTCCAGGCG 1698
QY 1346 CCCTGAACCGCGCAAGCTGACGAGGTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1405
Db 1589 GC---AGTGACCATCGGTGACAGCTTCGCGCGCTACGACAGCGGTACACCGCGCG 1745
QY 1406 GTGCCAGCGAGTGTTCGCGGCGGCGGCTACCCCGGAGAGTGGTSCCAACTGCATAGCC 1465
Db 1746 AGTCGCTGAGCGGCTGCGGACACCTGGGACGAGCGCTGCGGCGCAACTTCAACACG 1805
QY 1466 AGGACCTGTCTGTCTCAAGCCCGCCAGAGTGGGAGGCGCTGCTGAGGAGTGGTGT 1525
Db 1806 TCCGAAGCTCAAGGCGCAAGTACCCGACATCAAGGTCTCTGTCTTCGCGGCGCTGA 1865
QY 1526 ACGGCAAGGCGGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1559
Db 1866 CTGTGTCGCGGCTTCACCGACGCGGTGAAGA 1899

RESULT 12

US-09-294-093B-3520
; Sequence 3520, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 3520
; LENGTH: 299
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700380278H1
; LOCATION: 118
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-3520

Query Match 4.5%; Score 72.2; DB 10; Length 299;
Best Local Similarity 60.1%; Pred. No. 2.2e-08;
Matches 119; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 1130 AGTACAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1189
Db 75 AATACCATGGCGGAGTGAAGTATGCTTAAGCTATGACGAGCGGCTGTCACATTTGATAT 134
QY 1190 CGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1249
Db 135 ATGCTGGCGGAGACTTCAATTCGTTCTTCACTTCACTTCACTTCACTTCACTTCACT 194
QY 1250 TGCAGCGCATGACATACGCTACCGTGCCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1309

Db 195 TTATGTCTATGCGCTATGATCCATCCAGTTGTTTCGAAAACTGGAGGCGCTGTACGACA 254
QY 1310 CCGTCAAGGAGGCGGTCA 1327
Db 255 CCGTTTTTCAATGTCGACA 272
RESULT 13
US-09-894-633A-83
; Sequence 83, Application US/09894633A
; Patent No. US20020124285A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRE
; FILE REFERENCE: 38-21(15856)B
; CURRENT APPLICATION NUMBER: US/09/894,633A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 60/214,357
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 09/894,633
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 83
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Zea mays
US-09-894-633A-83

Query Match 4.5%; Score 72.2; DB 10; Length 824;
Best Local Similarity 47.6%; Pred. No. 2.2e-08;
Matches 246; Conservative 0; Mismatches 268; Indels 3; Gaps 1;
QY 795 CGTATCCGCGCCCAAGGCGCATTTGAGGCGCATTTGACGCGCATTTGAGAGTGGAA 854
Db 132 CTTGCTGCTGCTGCTTTCTTCCAGAGTGTCTTCTCAGCGGGTTCGACGCGTGTGAT 191
QY 855 CCCCAGACGCGCAAGATTCCTCTGCGCCCTACAGCAGACAGCGTGTACGCGGCA 914
Db 192 CGCTCCACCCAGTTCAGAGTCCGAGCAGCAGCGGAGATCAACCACTCCCTCCCGG 251
QY 915 GCGCGCGCGCAAGAGGCGCTTCAGCGCGAGTGGGCGGCTGTGGGCGGCTGTGGACCCACGCGCC 974
Db 252 GGACGCTTCGACGCGCGTGTGCGGCGCAAGCTGCGCCCTGGAGCTGGAGTGGCGCGGT 311
QY 975 CTTGTTCGCTTCATCGCGCGCTGGAGGAGCAGAGGCTGTGGACATCATCTGGCGCC 1034
Db 312 GGTGT---CCTGCGCGCATCTCGACTGCGGTGCGGCGGTGTGATTTACCATACCG 368
QY 1035 CTTGCCCAAGATCTCTGGCGACCCCAAGGTGACATGCGCATCTCTGGGTACCGGAAGC 1094
Db 369 CGGCGCGCGGTACCGCGTTCCGCTGGGCGCGAGGAGTCTGCTGCTGCTGCGCCACGCG 428
QY 1095 CGCCTACGAGAGCTGGTGAACCCATCGGCAACCAAGTACAGGCGCGCGCAAGGCGT 1154
Db 429 GCGCGCGGTGGAGTGGCGGCGCAACTTCACTGCGGCGGCGGCGGCGGCGGCGGCGG 488
QY 1155 GGTCAAGTTCTCGGCGCGCTTGGCGCATGTCTACCGCGCGCGGCGGCGGCGGCGGCT 1214
Db 489 CGCAGAGGTTTACGGTTCAGAGTGTGGCGGTGTGGCGGTGTCCGCGCGCCACGCTGGCT 548
QY 1215 GCGCTCGGCTTCGAGCGCTTCGCGGCTGTATTCAGCTGACGCGCATGCTAGCTACCGT 1274
Db 549 CTCCTCACTCAAGAGGTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 608
QY 1275 GCGCGTGTAGCTCCACCGCGGCTGTGTGACACC 1311
Db 609 GGAGCAGTTTCGACCCCGCATGAACTCCGCTTCACGCC 645

RESULT 14

US-09-934-900-11
; Sequence 11, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Zea mays
US-09-934-900-11

Query Match 4.4%; Score 70.8; DB 9; Length 1415;
Best Local Similarity 44.8%; Pred. No. 4.9e-08;
Matches 316; Conservative 0; Mismatches 387; Indels 3; Gaps 1;

QY	712	GCCGCCGACAACTGGTGTGTCGCCCACTACGCGGAGCGGAGATCGCTGCCGATGCC	771
DB	346	GCGACATCTCCCGGACTCTCTCGAGATGTTCCGGCAGGATCCGCGAGTCGCG	405
QY	772	GCCGGCGGTGTGGAGTGGACACCGCTCATCCGCCCAAGGCAATGAGGCAATGTGAAC	831
DB	406	GCCCGCGCGGGGGCTCCCGGACGAGTACTCTGTCGTCGTGGGGGACATGGTCACG	465
QY	832	GGCATGACATGAGGAGTGAACCCCAAGACCAAGTTCCTGTCGTGCGCCCTACGAC	891
DB	466	GAAGAGGCGCTGCCACGTACACGACCATGATCAACAGCTCGACGGCTCCGGACGAG	525
QY	892	CAGAACAGCTGTACGCGCGGCAAGCGCGCCCAAGGAGGCGCTTCAGGCGGAGCTGGC	951
DB	526	ACGGCGCCAGCACTCCCTGGGGGTCTGGAGCGCGCTTGACCGCGGAGAGAAC	585
QY	952	CTGCGCTGTGACCCCAACCGCCCCCTGTTCGCTTCATCGCCCGCTGGAGGAGCAGAAG	1011
DB	586	CGCCACGCGGACATCTCTCGGCAAGTACATGTACCTATCCGSCGCGTCGACATGGCATG	645
QY	1012	GGTGTGACATATCTTCGCGCGCTCCCAAGATCTTGGCCACCCCGCAAGTGCAGATC	1071
DB	646	GTGAGAGACCGTCCAGTACCTCATCGGTCCGGCATGTATCCCGAACGAGAACAAAC	705
QY	1072	GCCATCTGTGGTACCGGCAAGCGCGCTACGAGAAGCTGTGTAAGCCATCGGACCAAC	1131
DB	706	CCGTACCTGGCTTCGTGTACACAGCTTCCAGAGCGCGGAGCGCGCTTCGACGCG	765
QY	1132	TACAAGGCGCGCAAGGCGGTGTCAACTTCTCGCGCCCTTGGCGGCATCTCAACC	1191
DB	766	AACACCGCGCGGTTCGCGGCGCAGGCGACGACGCTCTGGCGCGGCTTCGGGCACC	825
QY	1192	GCGGCGCGGCTTCATGCTGTGTGCTTCGCGCTTCGAGCGCTTCGCGGCTTCGAGCTG	1251
DB	826	ATCGCGCGCGGAGAGAGAGGAGCAGGAGCGCGGTACGCGGCGATCTGTCGACGCTGCT	885
QY	1252	CACGCCATGACATACGATACGTCGCGCTGTGTAGCTTCCACCGCGGCTGGTGCACAC	1311
DB	886	CAGTGCACCGGAGGCGCGGTGCTCGCGTTCGCGACATGATGCGCAAGCGGATCACC	945
QY	1312	GTCAGAGGCGGTACCGGCTTCCACATGGGCGGCTTGAACCCCGCAAGCTGGACGAG	1371
DB	946	ATGCGCGCGCACTCA---TGCACGAGGCGCGGACATGATGACCTGTTCGACACTTCGC	1002

QY	1372	GCTGACGCGGACGCGCTGCGCCGACCGCTGCGCGCTGCGCGGAGG 1417
DB	1003	GCGCTCGCCGACGCGCTGCGCTGTACACCGCGCGGACTACGCGG 1048

RESULT 15
US-09-988-462-6
; Sequence 6, Application US/0988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/988,462
; FILING DATE: 20-NO. US20030046726A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/547,422
; FILING DATE: 11-APR-2000
; APPLICATION NUMBER: US 08/459,504
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3621
; OTHER INFORMATION: /product= "Full-length, maize
; optimized cryiB"
; /note= "Disclosed in Figure 6."
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-988-462-6

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run On: June 4, 2003, 13:49:45 ; Search time 28.1631 Seconds
(without alignments)
2512.365 Million cell updates/sec

Title: US-09-980-771A-9
Perfect score: 2769
Sequence: 1 ALDIVMAEAEVAPWSKTGL.....GGVATAKKEIKVPAEKIP 531

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1440	52.0	606	AA25476	Granule-bound star
2	1397.5	50.5	609	AAW56485	Oryza sativa starch
3	1390	50.2	527	AA25476	Arabidopsis thaliana
4	1390	50.2	563	AA25476	Arabidopsis thaliana
5	1390	50.2	610	AA25476	Arabidopsis thaliana
6	1390	50.2	610	AA25476	Arabidopsis thaliana
7	1353.5	48.9	533	AAW56484	Herbicide-activated
8	1344.5	48.6	637	AAW56484	Herbicide-activated
9	1331.5	48.1	502	AA25476	Protein encoded by
10	904	32.6	534	AA25476	Central fragment of

11	898	32.4	792	23	ABB92160	Herbicide-activated
12	891.5	32.2	647	20	AAW09004	Wheat starch solub
13	882.5	31.9	649	19	AAW38218	Maize starch synth
14	878	31.7	671	19	AAW23937	Maize starch synth
15	878	31.7	756	21	AAW50818	Wheat soluble star
16	873.5	31.5	626	15	AAW51231	Herbicide-activated
17	870.5	31.4	652	23	ABB93595	Soluble rice starch
18	861.5	31.1	539	19	AAW56491	Herbicide-activated
19	861.5	31.1	583	19	AAW56488	Zea mays starch sy
20	852.5	30.8	583	19	AAW70894	Zea mays soluble s
21	847	30.6	802	23	AAU99845	Maize starch solub
22	847	30.6	813	23	AAU99844	Modified barley st
23	846	30.6	812	23	AAU99847	Barley cultivar Mo
24	845	30.5	804	19	AAW70892	Barley line MK6927
25	844	30.5	798	21	AAW37566	Maize starch solub
26	842	30.4	799	21	AAW37567	Wheat starch synth
27	842	30.4	799	21	AAW37597	Wheat starch synth
28	841	30.4	799	21	AAW23938	Wheat starch synth
29	837	30.2	698	19	AAW56487	Wheat granule-boun
30	825.5	29.8	812	23	AAU99846	Zea mays soluble s
31	825	29.8	597	21	AAW37568	Barley line 292 st
32	767	27.7	466	23	AAW51865	Wheat starch synth
33	726	26.2	459	17	AAW99540	Rice starch synth
34	701.5	25.3	669	19	AAW70893	Soluble starch syn
35	701.5	25.3	669	19	AAW56486	Maize starch solub
36	669	24.2	483	23	ABB54012	Zea mays soluble s
37	647.5	23.4	476	23	ABP27592	Lactococcus lactis
38	593	21.4	238	22	AAW31175	Streptococcus poly
39	580	20.9	477	13	AAW25462	A granule bound st
40	580	20.9	477	13	AAW53890	giga. Escherichia
41	568.5	20.5	677	19	AAW99539	E. coli glycogen s
42	568.5	20.5	1230	18	AAW17785	Soluble starch syn
43	568.5	20.5	1230	21	AAW49306	Potato tuber solub
44	561.5	20.3	1025	23	ABB90967	Potato starch synt
45	546	19.7	495	19	AAW70885	Herbicide-activated

ALIGNMENTS

RESULT 1
RAR25476
ID AAR25476 standard; Protein; 606 AA.
XX
AC AAR25476;
XX
XX
DT 15-JAN-1993 (first entry)
XX
DE Granule-bound starch synthase of potato.
XX
KW GBSS gene; amylopectin; amylose production;
XX inhibition; promoter; antisense construct.
XX
OS Solanum tuberosum.
XX
XX
PN W09211376-A.
XX
XX
PD 09-JUL-1992.
XX
XX
PF 20-DEC-1991; 91WO-SE00892.
XX
XX
PR 21-DEC-1990; 90SE-0004096.
XX
XX
PA (AMYL-) AMYLOGENE HB.
XX
XX
PI Hofvander P, Persson PT, Tallberg A, Wikstrom O;
XX
XX
DR WPI; 1992-250096/30.
XX
XX
XX N-PSDB; AAQ26404.
XX
XX
PT Modifying potatoes to form amylopectin starch - using an
XX anti-sense construct to inhibit granule-bound starch synthase

Claim 6; Page 28-33; 46pp; English.

PS A genomic library in EMBL3 was prepared using leaves of the potato
 XX Blintje. The library was screened with cDNA clones for the 5' and 3'
 CC ends of the GBSS gene. A full-length clone of potato GBSS gene was
 CC identified (wx311) and isolated from the genomic library. The gene
 CC contained 12 introns. The amino acid sequence was deduced from it.
 CC Three fragments of the full-length sequence (5'-end, middle and
 CC 3'-end sequences) were characterised as suitable for use in novel
 CC antisense constructs to suppress amylose formation in potatoes.
 CC See also Q28400-3.

XX Sequence 606 AA;

Query Match 52.0%; Score 1440; DB 13; Length 606;
 Best Local Similarity 53.5%; Pred. No. 9.1e-116;
 Matches 292; Conservative 67; Mismatches 145; Indels 42; Gaps 10;
 QY 2 LDIVMAAEVAPWSKTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVYDI- 60
 Db 81 MNLIFVTEVGPWSKTGELGDLGPPALAAARGHRVMTISPRYDQYKDAWDTGVAVEVK 140
 QY 61 MG---EKVRPHSIKKGVRHVDHPFLAKVWGKTSKLYGPRSGADYLDNHRKRFALFC 117
 Db 141 VGSISIEIVRFHCYKRGVDRFVDHPMELEKVGKTSKLYGPRSGADYLDNHRKRFALFC 200
 QY 118 KAAEAAARVLPE-----GP-GEDCVFVANDHWSALVPVLLKDEYQPKGQFTKAKSVLA 169
 Db 201 QAALEAPRLNLNNSNFSGYGEDVLFANDHWTALIPCYLKSMSYSGIYLNKAVAF 260
 QY 170 IHNIAFOGRWEEAFKDKLPQAAFDKLAFLSDGSAKYVTEATPMEDEKPLTGKTKYKI 229
 Db 261 IHNIAFOGRWEEAFKDKLPQAAFDKLAFLSDGSAKYVTEATPMEDEKPLTGKTKYKI 302
 QY 230 NWLKGIIAADKLVTSVPNATEIAADAAGGVLDTVIRAKIGEVNGMDIEENPKTD 289
 Db 303 NWMKAGILEADKLVTSVPNATEIAADAAGGVLDTVIRAKIGEVNGMDIEENPKTD 362
 QY 290 KFLSAPYDQNSVYAGKAAKAAKALQALQELGDPDPTAPLFAFAGRLGEEQKGVDIILALPKI 349
 Db 363 KYTDVKYDITVMDAKPILKEALQAAVGLPVDKXIPILGIFIGRLGEEQKGVDIILALPKI 422
 QY 350 LATPKVQIATLGTKAAEKLVAIGTKYKRAKGVKFSAPLAHMLTAGADFMVPSRF 409
 Db 423 IGL-DVQITVLGIGTKKEFEQIEQLEVLNPNKAKGVAKFNVPPLAHMLTAGADFMVPSRF 481
 QY 410 EPCGLIOLHAMHYGTVPVWASTGGLVDTVKGVTFGFMGALNP--DKLDEADADALAAATV 467
 Db 482 EPCGLIOLHAMHYGTVPVWASTGGLVDTVKGVTFGFMGALNP--DKLDEADADALAAATV 541
 QY 468 RRASEVFAAGGRYPPEMVANCIQSGLSWSPKPAQKWEGLL-----EEVYKGGVATAK 519
 Db 542 ARALAVYGTLLAFAEIKNMCSEELSWKEPAKKWETLLGLGASGSEPGVEGE-ETAPLAK 600
 QY 520 EEIKVP 525
 Db 601 ENVATP 606

RESULT 2

AAW56485

ID AAW56485 standard; Protein: 609 AA.

XX AAW56485;

AC AAW56485;

XX 11-SEP-1998 (first entry)

DE Oryza sativa starch (bacterial glycoen) synthase.

XX SER; starch-encapsulating region; fusion vector;

KW starch synthase; bacterial glycoen.

XX Oryza sativa.

OS

XX WO9814601-A1.

XX 09-APR-1998.

XX 30-SEP-1997; 97WO-US17555.

XX 30-SEP-1996; 96US-0026855.

XX (EXSE-) EXSEED GENETICS LLC.

XX Guan H, Keeling P;

XX WPI; 1998-240100/21.

XX N-PSDB; AAV29753.

XX Hybrid polypeptide comprising starch-encapsulating region and

XX protein, -useful for, e.g. producing protein(s) resistant to

XX degradation by stomach acids

XX Example 2; Page 32; 156pp; English.

XX The sequence is that of starch (bacterial glycoen) which is

XX encoded by the waxy gene. It can be used in the production of a hybrid

XX polypeptide comprising a starch-encapsulating region (SER) fused

XX to a payload protein. The hybrid polypeptide can be used to make

XX modified starches comprising the payload protein, selected from,

XX e.g. hormones, growth factors, antibodies, enzymes, dyes,

XX immunoglobulins, etc. The modified starch can also be used

XX to provide grain feeds enriched in amino acids. By encapsulating

XX the payload protein in starch, it is more resistant to

XX degradation by stomach acids.

XX Sequence 609 AA;

Query Match 50.5%; Score 1397.5; DB 19; Length 609;

Best Local Similarity 51.4%; Pred. No. 4.4e-112;

Matches 281; Conservative 76; Mismatches 147; Indels 43; Gaps 9;

QY 2 LDIVMAAEVAPWSKTGGGLDVTGGLPIELVKRGHRVMTIAPRYDQYADAWDTSVVYDI- 60

Db 83 MNVFEVGAEMAPWSKTGGGLDVTGGLPPAMAANGHRVMVISPRYDQYKDAWDTSVVYAEIK 142

QY 61 ---MGEKVRPHSIKKGVRHVDHPFLAKVWGKTSKLYGPRSGADYLDNHRKRFALFC 117

Db 143 VADRYERVRPHSIKKGVRHVDHPFLAKVWGKTSKLYGPRSGADYLDNHRKRFALFC 202

QY 118 KAAEAAARVL-----PFGP---GDCVFVANDHWSALVPVLLKDEYQPKGQFTKAKSVLA 169

Db 203 QAALEAPRLNLNNSNFSGYGEDVLFANDHWTALIPCYLKSMSYSGIYLNKAVAF 262

QY 170 IHNIAFOGRWEEAFKDKLPQAAFDKLAFLSDGSAKYVTEATPMEDEKPLTGKTKYKI 229

Db 263 IHNIAFOGRWEEAFKDKLPQAAFDKLAFLSDGSAKYVTEATPMEDEKPLTGKTKYKI 305

QY 230 NWLKGIIAADKLVTSVPNATEIAADAAGGVLDTVIRAKIGEVNGMDIEENPKTD 289

Db 306 NWMKAGILEADKLVTSVPNATEIAADAAGGVLDTVIRAKIGEVNGMDIEENPKTD 365

QY 290 KFLSAPYDQNSVYAGKAAKAAKALQALQELGDPDPTAPLFAFAGRLGEEQKGVDIILALPKI 349

Db 366 KYITAKYDITVMDAKPILKEALQAAVGLPVDKXIPILGIFIGRLGEEQKGVDIILALPKI 425

QY 350 LATPKVQIATLGTKAAEKLVAIGTKYKRAKGVKFSAPLAHMLTAGADFMVPSRF 409

Db 426 M-OEDVQIVLLGIGTKKEFEQIEQLEVLNPNKAKGVAKFNVPPLAHMLTAGADFMVPSRF 484

QY 410 EPCGLIOLHAMHYGTVPVWASTGGLVDTVKGVTFGFMGALNP--DKLDEADADALAAATV 467

Db 485 EPCGLIOLHAMHYGTVPVWASTGGLVDTVKGVTFGFMGALNP--DKLDEADADALAAATV 544

QY 468 RRASEVFAAGGRYPPEMVANCIQSGLSWSPKPAQKWEGLL-----VATAK 518

Db 545 KRAIKVGTPAYEEMVRNMCNODLSWKGPKNWNL--LGLGVAGSAGCIEGDEIAPLA 602
QY 519 KEEIKVP 525
Db 603 KENVAAP 609

RESULT 3
AAG04668
ID AAG04668 standard; Protein; 527 AA.
XX
AC AAG04668;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 782.
DE
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 24-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 08-JUN-1999; 99US-0137724.
PR 10-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 99US-0139452.

PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0143977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.

PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144086.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0132048.
PR 21-JUL-1999; 99US-0132407.
PR 21-JUL-1999; 99US-0132484.
PR 22-JUL-1999; 99US-0132485.
PR 22-JUL-1999; 99US-0132486.
PR 22-JUL-1999; 99US-0132487.
PR 22-JUL-1999; 99US-0132488.
PR 22-JUL-1999; 99US-0132489.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148441.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.

Db 480 FEPGLIQLQGMRYGTPCACASTGGGLVDFTIEGKTGFHMGRLSDCNVVEPADVKKVATT 539
 QY 467 VRRASVFAGRGYPNVAACISODLSWSKPAQWEGLEE--VYCKGGV-----ATAKK 519
 Db 540 LQRAIKVGTGPAYEEMVRNMIQDLSWKGPARNWENVLISLVAGGEPGVGEIEIAPLAK 599
 QY 520 EEIKVP 525
 Db 600 ENVAAP 605
 RESULT 9
 AAR25474
 ID AAR25474 standard; Protein; 502 AA.
 AC AAR25474;
 DT 15-JAN-1993 (first entry)
 XX Central fragment from potato GBSS.
 DE Granule-bound starch synthase; amylopectin; amylose production;
 KW inhibition.
 XX Solanum tuberosum.
 OS WO9211376-A.
 PN 09-JUL-1992.
 PD 20-DEC-1991; 91WO-SE00892.
 XX 21-DEC-1990; 90SE-0004096.
 XX (AMYL-) AMYLOGENE HB.
 PA Hofvander P, Persson PT, Tallberg A, Wikstroem O;
 PI WPI; 1992-250096/30.
 DR N-PSDB; AAQ26401.
 XX Modifying potatoes to form amylopectin starch - using an
 PT anti-sense construct to inhibit granule-bound starch synthase
 XX Claim 1; Page 21; 46pp; English.
 CC A genomic library in EMBL3 was prepared using leaves of the potato
 CC Bintje. The library was screened with cDNA clones for the 5' and 3'
 CC ends of the GBSS gene. A full-length clone of potato GBSS gene was
 CC identified (wx311). A BglII-SpeI fragment ("m") of the clone was
 CC found to contain the central region of the gene and was cloned in
 CC pUC13 to give pSm. Restriction of pSm with NsiI and HpaII gives
 CC fragment II which was cloned in pJRD184 to give pJRDm11. Further
 CC restriction of pJRDm11 with HpaI-SstI gives a 2549bp fragment
 CC comprising exons and introns from the middle of the gene. The
 CC fragment can be used to make antisense constructs to suppress amylose
 CC formation in potatoes. See also Q26400-4.
 XX Sequence 502 AA;
 SQ
 Query Match 48.1%; Score 1331.5; DB 13; Length 502;
 Best Local Similarity 55.6%; Pred. No. 1.7e-106;
 Matches 269; Conservative 55; Mismatches 125; Indels 35; Gaps 9;
 QY 2 LDIVMAAEVAPWKSCTGGTGLDVTGGLPIELVKRGHVMTIAPRYDQYADAMDTISVVDI- 60
 Db 39 MNLIFVTEVGPWKSCTGGTGLDVTGGLPPLAARGHVMTISPRYDQYKDAWDTGVAVEVK 98
 QY 61 MG---EKVYFHSITKKVYHVRWIDHPWFLAKVWGTGSKLYGPRSGADYLDNKKRFALPC 117
 Db 99 VGDSTIEIVREFHCYKRGVDRVFDHPMFEKVGWGTGSKLYGPRAGLDYLDNELRFLIC 158
 QY 118 KAAIEAARVLFP-----GP-GEDCVFANDWHSALYPLVLLKDEYQPKQFTKAKSVLA 169

Db 159 QAAALEAPKVLNLSNYSFYSGYGEDVLFITANDHTALIPCYLKSMTOSRGIYNKAVFC 218
 QY 170 IHNIAFQGRWEEAFKDTKLPOAAAFKLFASDGYAKVYVTEATPMEDEKPLTGKTKYKI 229
 Db 219 IHNIAQGRFSFDFLLNLPDEFGRSFDIDGY-----PVKG--RKI 259
 QY 230 NWLKGIIAADKLIVTSPNYATEIADAAGGVELDTVIRAKGTIEGVNGMDIEWNPXTD 289
 Db 260 NNMKAGILESHRVTVSPYQAELVSPVHRGVELDSVLRKTCITGVNGMDTOENPATD 319
 QY 290 KFLSAPVD--QNSVYAGKAAKEALQAEGLPVDPTAPLFAFIEGRLEQKGVDIILAAALPK 348
 Db 320 KYTDVYDITTOVMDAKPLLEKALQAAVGLPVKKIPLIGFIEGRLEQKGSILVLAHLK 379
 QY 349 ILATPKVQIAIILGTGKAAAYEKLVNAICTYKGRAGVVKFSAPLAHMLTAGADPMLVPSR 408
 Db 380 FIGL-DVOIVVLGTGKKEFEQLEVLVYPNKAGVAKENVPLAHMITAGADPMLVPSR 438
 QY 409 FEPGLIQLHAMHYGVTVVASTGGLVDTVKESYTGFMHGAALNP--DKLDEADADALAAT 466
 Db 439 FEPGLIQLHAMRYGTVPICASTGGLVDTVKESYTGFMHGAALNP--DKLDEADADALAAT 498
 QY 467 VRRR 470
 Db 499 VARA 502
 RESULT 10
 AAB49307
 ID AAB49307 standard; Protein; 534 AA.
 AC AAB49307;
 DT 01-MAR-2001 (first entry)
 XX Wheat starch synthase GBSS protein.
 DE Wheat; starch synthase; SSII; SSIII; starch content; starch synthesis;
 KW food product; adhesive.
 XX Triticum aestivum.
 OS WO2000066745-A1.
 PN 09-NOV-2000.
 PD 28-APR-2000; 2000WO-AU00385.
 XX 29-APR-1999; 99AU-0000052.
 PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (GOOD-) GOODMAN FIELDER LTD.
 PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
 XX Morell M, Li Z, Rahman S, Appels R;
 XX WPI; 2000-647602/62.
 DR Nucleic acid molecules encoding wheat starch synthase (WST)-I and
 PT WST-II, useful in modifying plant starch content and/or composition -
 XX Example 15; Fig 9; 21pp; English.
 CC The present invention relates to novel protein and coding sequences from
 CC wheat. The proteins are wheat starch synthases, designated SSII and
 CC SSIII. These can be used in the modification of plant starch content or
 CC composition, and to screen plants to identify mutations which affect
 CC starch content and composition. The starch can then be used in food
 CC products, such as flour, and in films, coatings, adhesives, building
 CC materials and packaging materials.
 XX Sequence 534 AA;
 SQ

Query Match 32.6%; Score 904; DB 21; Length 534;
 Best Local Similarity 32.5%; Pred. No. 1.8e-69;
 Matches 213; Conservative 48; Mismatches 103; Indels 292; Gaps 9;

QY 7 VAAEVPWSTGGLGVTGGGLPIELVKGRHRYMTIAPRYDOYADAWDTSVVVDIMCEKVR 66
 DB 2 VGEAMAPWSTGGLGDLGLPPAMAANGHRVWVISPXDQYKDAWT----- 49
 QY 67 YFHSIKKGVRWIDHPFLAKWGTGSKLYGPRSGADYLDNHRKFALEFCRAALEAARV 126
 DB 50 -----LEKVRGKTEKIYDPDAGTDYEDNQRFSLCQAALVEPRI 90
 QY 127 I-----PF----- 129
 DB 91 LNLNDNPFYFCHNISIYGRFSFDFDFAQLNLPDRKSSFDITDGYDKPVEGRKISVWSEI 150
 QY 130 -----GP-GEDEVFVANDMHSALVPVLLKDEYOPK 158
 DB 151 KVDKYERVRVPHCYKRGVDRVVDHPCFSGPYGEDVFCVNDWHTGLLACLYLKSNYOSN 210
 QY 159 GQFTKAKSVLAHNIAFOGRWEEAFKDTKLPQAAFDKLAFLSDGYAKYITEATPMEDEK 218
 DB 211 GIYRAAKVA----- 219
 QY 219 PPLTGKTYKIKNLKGGIIAADKLVTSPPNVAETEAADAAGGVLDTVIRAKGIEGVNG 278
 DB 220 -----NWKAGILQADKLVITVSPYFAEELISGEARGCELDNIMRLTIGITTVNG 268
 QY 279 MDIEENPKTKFLSAPYDQNSVYAGKAAK----- 309
 DB 269 MDVSEWPTKDKFLAVNYDITTALEKALNEALKEGKALNKIKEEDVOIVILGTGKKFE 328
 QY 310 -----EALQAEGLPVDPTAPLFAFGRLEBQKGVDTILA 344
 DB 329 RLLKSIIEKFSKVRVVRNAPLAELALQAEVGLPVDKRVPLVAFVIGRLEBQKGPVMA 388
 QY 345 ALPKILATPKVQIAILGTGAAAEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADPML 404
 DB 389 SIPEI-----HOMAGADVIA 404
 QY 405 VPSFEPGGLIQLHAMHYGTPVVAAGGLVDTKEGVTGPHMGALNPD--KLDEADADA 462
 DB 405 VTSFEPGGLIQLQMGYGTGPCACASTGGLVDTIVEGKTGPHMGRSLVDCNVVFPADYK 464
 QY 463 LAATVRASEVFGAGRYPE-----WVANCISQDLSWSKPAOKWEGLLBEV 507
 DB 465 VVTLKRAVVGTPAYHEAPLAVENVAAPMVKNCMIQDLSWKGPAKNWEDVLEL 520

RESULT 11
 ID ABB92160
 AC ABB92160;
 XX ABB92160;
 DT 31-MAY-2002 (first entry)
 XX Herbicidally active polypeptide SEQ ID NO 1371.
 DE Herbicidal; plant; agriculture; herbicide.
 KW Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX Arabidopsis thaliana.
 PN W0200210210-A2.
 XX W0200210210-A2.
 PD 07-FEB-2002.
 XX 07-FEB-2002.
 XX 28-AUG-2001; 2001WO-EP09892.
 XX 28-AUG-2001; 2001WO-EP09892.
 XX (FARB) BAYER AG.

Tietjen K, Weidler M;
 WPI; 2002-269010/31.
 Identifying plant target proteins for herbicidally active compounds,
 comprising aligning and comparing nucleic acid or amino acid sequences
 from plant with nucleic acid or amino acid sequences from non-plant
 organisms -
 Claim 5; SEQ ID NO 1371; 261pp + Sequence Listing; English.
 The invention relates to identifying target proteins
 (AB990790-AB994016) for herbicidally active compounds, comprising
 aligning and comparing nucleic acid or amino acid sequences from plant
 with nucleic acid or amino acid sequences from non-plant organisms using
 suitable search parameters, where plant sequences having an E-value
 greater by a factor of 3 than the E-value of most similar non-plant
 sequences are selected. The polypeptides or nucleic acids encoding them
 are useful for identifying modulators. The identified modulators are
 useful as herbicides.
 Sequence 792 AA;
 Query Match 32.4%; Score 898; DB 23; Length 792;
 Best Local Similarity 40.5%; Pred. No. 1.1e-68;
 Matches 214; Conservative 81; Mismatches 174; Indels 60; Gaps 15;

QY 2 LDIVVAAEVPWSTGGLGVDVTGGPIELVKGRHRYMTIAPRYDOYADAWDTSV--VVD 59
 DB 301 MNVILVAAEVPWSTGGLGVDVAGALPKSLARRGHRVWVVPYAEYAEAKDLGVRKRYK 360
 QY 60 IMGE--KYRHSIKKGVRWIDHPFLAKWGTGSKLYGPRSGADYLDNHRKFALEFC 117
 DB 361 VAGQDMVYVYHAFIDGVDFVDFIDSEF-----RHLSNNIY---GGNRKLDILKRVVLC 411
 QY 118 KAAIEAARVLP-----FGPEDCVFVANDMHSALVPVLLKDEYQPKGQFTAKSVLAHNL 172
 DB 412 KAAVEVPWVPCGGVCGYGDG--NLAFIANDWHTALLPVYLKAYYRDHGMKTYRSLVITHN 470
 QY 173 IAFGRWEEAFKDTKLPQAAFDKLAFLSDGYAKYITEATPMEDEKPLTKYKKNWL 232
 DB 471 IAHGGRGVDDFSYVDLPSHYLDSFKLYD-----PVGGEHF---NIF 509
 QY 233 KGGIADKLVTSPPNVAETEAADAAGGVLDTVIRAKG--IEGTVNGMDIEEWNPKTDK 290
 DB 510 AAGLKAADRVLTSHGYSWEVKT--LEGGWGLHNIINENDWKFGRGIVNGIDTQWNPEDT 568
 QY 291 FLSAP---YDQNSVYAGKAAAEKALQAEGLPVDPTAPLFAFGRLEBQKGVDTILAAL 346
 DB 569 YLHSDDYTNYSLENLHIGKPCQAALQELGLPVRPDPVPLIGFICRLDQKGVLDIAEAV 628
 QY 347 PKILATPKVQIAILGTGKAAAEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADPMLVP 406
 DB 629 PWWW-SQDVQLVMLGTGRPDLEEVLRQMEHOYRDKRGWGVGFSVKTHRITAGADILMP 687
 QY 407 SRFEPCGLIQLHAMHYGTPVVAAGGLVDTKEGVTGPHMGALNPDKLDEADA 460
 DB 688 SRFEPCGLIQLYANNYGTIPVWVAVGGLRDVQVQFDYPSETGLGWTDSAGKLIHALG 747
 QY 461 DALAATVRASEVFGAGRYPEWVANCISQDLSWSKPAOKWEGLLBEVVY 509
 DB 748 NCL-LTYREXKESWEG-----LQRRGMTQDLSWDAEAEKVEEVLVAAYK 790

RESULT 12
 ID AAY09004
 AC AAY09004;
 XX AAY09004;
 DT 05-JUL-1999 (first entry)
 XX

Db 202 HIRPCFGGEHEVTFEHEYRSDVDFVDPHSY-----HRPGLNYGDKFGA-TGDNQFR 254
 QY 113 FALFCKAAIEARVLPFGP----GDCVFVANDHSAIVPVLLKDEYQPKGQFTAKSVIA 169
 Db 255 YTLICYAACEAPLVLELGGYTYGQNCMEFVNDHSAIVPVLLAARYGYGVYKDSRSILV 314
 QY 170 IHNIAFGRMWEEAFKDTKLPOAFAFDKLAFSGDKYAKVYTEATPMEDEKPLTKYK 229
 Db 315 IHNLAHOGVEPASTYPLGLPPEWYGALEW-----VPEWARHLDKG-----EAV 361
 QY 230 NLWKGIIADKLVTPSPNYATEIAADAAGGVLDTVI--RAKGIEGVNMDIEENPK 287
 Db 362 NFLKGAVTADRIVTVSGYSWEVTT-AEGGQGLNELLSRKSXVINGVINGIDINDNPA 420
 QY 288 TDFLSAPYQNSVYAKAAKAEALQAEGLPVDPDTAPLFAFTGRLEEQKGVDIILALP 347
 Db 421 TDKCIPCHYSVDDL-SGAKCKGALQELGLPIRPDVPFLIGFGRDLYQKGLDILQIIP 479
 QY 348 KILATPKVQIAILGTGKAAYEKLVAIGTKYGRAGKGVVKSAPLAHMLTAGADFMVPS 407
 Db 480 DLM-REDVQFVNLGSGDPELEDWNRSTESIFKDKFGRGVGFSVPVSHRITAGCDILLMP 538
 QY 408 RFPCGLIQLHAMHYGTVPVVASTGGVLDTVK-----EGVTGFHMGALNPKLDEA 458
 Db 539 RFPCGLNOLYAMGYGTVPVVHATGGLROTVENFENPFGEQGTGWAFAPLTEN---- 594
 QY 459 DADALATVRRASEVAGGR--YPEMVANCSQDLSKSPAKWEGILLE 505
 Db 595 ----MLWTLTAISTYREHKSSEGLMKRMSKDFTWDAARQYEIQF 639

RESULT 14

AAW23937
 ID AAW23937 standard; Protein; 671 AA.

AC AAW23937;
 XX

XX 21-MAY-1998 (first entry)
 XX

DE Wheat soluble starch synthase partial sequence.

KW Starch synthase; wheat; transgenic plant.

OS Triticum aestivum L. cv. Florida.

XX WO9745545-A1.

XX 04-DEC-1997.

XX 28-MAY-1997; 97WO-BF02793.

XX 11-SEP-1996; 96DE-1036917.

PR 29-MAY-1996; 96DE-1021588.

XX (AGRE) HOECHST-SCHERING AGREVO GMBH.

XX Block M, Loerz H, Luetticke S, Froberg C, Kossmann J;
 PI Walter L;

XX WPI; 1998-032652/03.

DR N-PSDB; AAV01527.

XX Nucleic acid encoding starch synthase enzymes from wheat - for
 PT transgenic plants that produce modified forms of starch, useful e.g.
 PT in foods, or for production of packaging materials and disposable
 PT goods

XX Claim 1; Page 47-50; 71pp; English.

XX This amino acid sequence comprises a near full-length sequence for
 CC a soluble starch synthase of summer wheat (cv. Florida). It was
 CC deduced from a cDNA clone (AAV01527) isolated from a 21-day carboxylis
 CC cDNA library. A granule-bound starch synthase (see AAW23938) has

CC also been identified. Isolated nucleic acids encoding these
 CC enzymes can be inserted into vectors for production of transgenic
 CC plants, particularly starch-producing plants, specifically wheat.
 CC Use of the isolated nucleic acids, or of antisense sequences, allows
 CC starch metabolism to be regulated in transgenic plants.
 CC Overexpression may result in improved crop yield, while modification
 CC of starch in planta may eliminate the need for subsequent
 CC chemical/physical modification. Plants with altered levels of the
 CC various isoforms of starch synthase will produce starch of different
 CC chain length, amylose/amylopectin ratio, degree of branching,
 CC phosphate content, gelatinisation behaviour, granule size and shape,
 CC viscosity etc. The starch produced by such plants is useful
 CC particularly in foods (especially bakery goods or pasta) or to
 CC produce packaging materials or disposable goods, as well as in any
 CC other known use of starch.

XX Sequence 671 AA;

Query Match 31.7%; Score 878; DB 19; Length 671;
 Best Local Similarity 39.9%; Pred. No. 4.5e-67;
 Matches 210; Conservative 78; Mismatches 164; Indels 74; Gaps 16;

QY 4 IVMVAAEVAPSKTGGIGDVTGGPIELVKGHRVMTIAPRY-----DQYADAWDTSVV 57
 Db 56 IVFVTGEAAPYAKSGGIGDVCGLFIALAARHVRVMPVRYLNGSSDKNTAKALYAKH 115
 QY 58 VDIM---GEKRVYFHSIKGVHRVWIDHPWFLAKVKGKTKLYGPRSGADYLDNHRF 113
 Db 116 IKIPCFGSHVETFEHYRDNVDWVVDHP-----SYHRPGS-LYGNFGA-FGDNQFR 168
 QY 114 ALFCKAAIEARVLPFGP---GEDCVFVANDHSAIVPVLLKDEYQPKGQFTAKSVIA 170
 Db 169 TLLCYAACEAPLVLELGGYTYGQNCMEFVNDHSAIVPVLLAARYGYGVYRDSRSLV 228
 QY 171 HNTAFQGRMWEAFKDTKLPOAFAFDKLAFSGDKYAKVYTEATPMEDEKPLTKYK 230
 Db 229 HNLAHOGVEPASTYPLGLPPEWYGALEW-----VPEWARHLDKG-----EAVN 275
 QY 231 WLKGGIIADKLVTPSPNYATEIAADAAGGVLDTVI--RAKGIEGVNMDIEENPK 288
 Db 276 FLKGAVTADRIVTVSGYSWEVTT-AEGGQGLNELLSRKSXVINGVINGIDINDNPT 334
 QY 289 DKFLSAPYQNSVYAKAAKAEALQAEGLPVDPDTAPLFAFTGRLEEQKGVDIILALP 348
 Db 335 DKCLPHYSVDDL-SGAKCKAELQELGLPVREDVPLIGFGRDLYQKGLDILKMAIPE 393
 QY 349 ILATPKVQIAILGTGKAAYEKLVAIGTKYGRAGKGVVKSAPLAHMLTAGADFMVPS 408
 Db 394 LM-REDVQFVNLGSGDPIFGWRMSTESSYKDKFGRGVGFSVPVSHRITAGCDILLMP 452
 QY 409 FEPCGLIQLHAMHYGTVPVVASTGGVLDTVK-----EGVTGFHMGALNPKLDEA 459
 Db 453 FEPCGLNOLYAMGYGTVPVVHGTGGLDRTVETNPFGAKGEGTGAFSPLTVDKMLWA 511
 QY 460 ADALATVRRASEVAGGRYPPEMVANCSQDLSKSPAKWEGILLE 505
 Db 512 -----LRTAMSTFRE-----HKPS--WEGIMK 531

RESULT 15

AAY50818
 ID AAY50818 standard; Protein; 756 AA.

AC AAY50818;

XX 18-FEB-2000 (first entry)

XX Wheat soluble starch synthase protein.

XX Soluble; starch synthase; wheat; transgenic plant; starch production;
 KW food; baking; pastry; packaging material; glucose; glucan; paper; pulp;
 KW adhesive; textile; building material; soil stabilizer; wetting agent;
 KW fertilizer; plant-protection; cosmetic; flocculant.

QY 349 ILATPKVOTAILGTGKAAEYKLYNAICTKYKRAKGVVKTSAPLAHMLTAGADFMVPSR 408
Db 479 LM-REDVQFVYMLGSDPIFEQWNRSTESSYKDKFRGWGVSFVPSVSHRITAGCDLLMPSR 537
QY 409 FEPCGLIQLHAMHYGTVPVASTGGGLVDIVK-----EGVTGFHMGALNPKLDEAD 459
Db 538 FEPCGLNOLYAMOYGVVPHVHGTGGGLRDIVETNPFCAKGEESTGWAFFSPLTVDKMLWA- 596
QY 460 ADALAATVRRASEVFAGGRYPEMVANCISQDLNSKSPAKQWEGILLE 505
Db 597 -----LRTAMSTFRE-----HKPS--WEGIMK 616

Search completed: June 4, 2003, 14:52:32
Job time : 32.1631 secs

XX Triticum aestivum.
XX DEL9820607-Al.
XX 11-NOV-1999.
XX 08-MAY-1998; 98DE-1020607.
XX 08-MAY-1998; 98DE-1020607.
XX (AGRE) HOECHST-SCHERING AGREVO GMBH.
XX Loerz H, Luetticke S, Block M;
XX WPI; 2000-024508/03.
XX N-PSDB; AAZ24487.
XX New enzyme with starch synthase activity, useful for producing starch
XX for foods and packaging materials -
XX Claim 1a: Page 19-21; 24pp; German.
XX This invention describes a novel protein (I) with the activity of wheat
XX starch synthase. Transgenic plants, specifically wheat, that contain (I)
XX are used for production of starch, used particularly in foods,
XX particularly baked and pastry goods and for making packaging materials or
XX disposable items. Starch may also be used as starting materials for
XX glucose or glucan components (e.g. for fermentation or further chemical
XX conversion); in paper and pulp production, as adhesives, in textiles,
XX in preparation of gypsum-based building materials, as soil stabilizer,
XX as wetting agent etc. in fertilizer and plant-protection compositions,
XX as binder (in pharmaceuticals, cosmetics, coal briquetting and casting
XX sand), as flocculant in soil or coal slurries, as rubber and leather
XX additives, and for production of synthetic polymers, e.g. polyurethane
XX films. Transgenic plants with increased/decreased production of (I)
XX produce starches with altered physical and/or chemical properties such as
XX amylose/amylopectin ratios, degree of branching, mean chain length,
XX phosphate content, gelatinization properties, gel- or film-forming
XX properties, or starch grain size or structure. This sequence represents
XX the soluble starch synthase isolated from wheat (Triticum aestivum L. cv.
XX Florida).
XX Sequence 756 AA;
Query Match 31.7%; Score 878; DB 21; Length 756;
Best Local Similarity 39.9%; Pred. No. 5.4e-67;
Matches 210; Conservative 78; Mismatches 164; Indels 74; Gaps 16;
QY 4 IVVYAAEYAPWSKGTGLGDTGGLPIELVKRGHVRMTIAPRY-----DQYADAWDTSVV 57
Db 141 IVFVTGEAAPYAKSGGLDVGSLPIALAARGHRVMVMPRYLNGSSDKNYAKALYAKH 200
QY 58 VDIM-----GEKVRFHSTIKGVHVRWIDHPWFLAKVWGKTGSKLYGPRSGADYLDNHRKF 113
Db 201 IKIPCFGSGHEVTFEHEYRONVDWVFDHP-----SYHRPGS-LYGDNFGA-FGDNQFRY 253
QY 114 ALFCKAATEARVLPFGP---GECVVFVANDWSHSAVLLKDEYQPKGQFTKAKSVLAI 170
Db 254 TLLCYACEAPLILLEGYIYQNCMFVNDWHSASLVPVLLAAKYRYPGYVEDSKSTLVI 313
QY 171 HNIAPQGRMWEAFKDKLPQAFDKLAFSDGYAKVYATPMEDEKPLPTGKTYKKIN 230
Db 314 HNLAHQGVPEASTYDGLGLPPEWYGALEW-----VFPWARHRLDXG-----EAVN 360
QY 231 WLKGIITADKLVTPSNFATFETIADAAGGVELDTVI--RAKGTIEVINGMDIEPWEKPT 288
Db 361 FLKGAVTADRTVTSQYSWEVTT-AEGGGLNELLSRSKSVLNGVINGIDINDWNETT 419
QY 289 DKFLSAPYDONSVAAGKAAKEALQAEGLPDEPTAPLFAFGRLEEOKGVDDIILAALPK 348
Db 420 DKCLPHHYSVDL-SGKAKKAEQLQELGLPVRDVPVPLIGFLGRDLYOKGIDLIKWAPE 478

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 4, 2003, 14:47:01 ; Search time 13.7251 Seconds
(without alignments)
3719.278 Million cell updates/sec

Title: US-09-980-771A-9
Perfect score: 2769
Sequence: 1 ALDIVMAAEVAPWSKTGGL.....GGVATAKKEIKVPAEKIP 531

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1481.5	53.5	608	S43341	starch synthase (E
2	1457.5	52.6	607	YUPOY	starch synthase (E
3	1415.5	51.1	603	S61504	glycogen(starch) s
4	1412.5	51.0	608	T10906	starch synthase (E
5	1398.5	50.5	609	JQ0703	glycogen(starch) s
6	1397.5	50.5	609	S11481	glycogen(starch) s
7	1395.5	50.4	603	YUBHY	glycogen(starch) s
8	1390	50.2	610	F86453	granule-bound star
9	1362	49.2	615	YUTWY	glycogen(starch) s
10	1355.5	49.0	608	T14731	glycogen(starch) s
11	1353.5	48.9	605	S07314	glycogen(starch) s
12	902.5	32.6	641	T07668	glycogen(starch) s
13	873.5	31.5	626	JQ2322	starch synthase (E
14	872	31.5	732	T01208	starch synthase (E
15	871	31.5	752	S61505	starch synthase (E
16	866	31.3	610	T06280	glycogen(starch) s
17	861.5	31.1	622	T01414	probable starch sy
18	847.5	30.6	788	T07667	starch synthase (E
19	839	30.3	491	T06798	glycogen(starch) s
20	837	30.2	698	T09130	probable starch sy
21	684.5	24.7	477	B95139	starch synthase (E
22	683.5	24.7	477	T098000	starch synthase (E
23	677.5	24.5	484	S40051	starch synthase (E
24	669	24.2	483	C86712	starch synthase (E
25	652	23.5	480	H98228	glycogen synthase
26	652	23.5	480	H98228	glycogen synthase
27	651	23.5	486	A73057	glycogen synthase
28	637	23.0	477	A97176	glycogen synthase,
29	622	22.5	484	F82165	glycogen synthase

ALIGNMENTS

RESULT 1

S43341

starch synthase (EC 2.4.1.21) precursor - cassava

N:Alternate names: bacterial-glycogen synthase; glycogen synthase; starch synthase

C:Species: Manihot esculenta (cassava)

C>Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2002

C:Accession: S43341

R:Salehuzzaman, S.N.I.M.; Jacobsen, E.; Visser, R.G.F.

Plant Mol. Biol. 23, 947-962, 1993

A:Title: Isolation and characterization of a cDNA encoding granule-bound starch synth

A:Reference number: S43341; MUID:94083565; PMID:8260633

A:Accession: S43341

A:Molecule type: mRNA

A:Residues: 1-608 <SAIL>

A:Cross-references: EMBL:X74160; NID:g437041; PIDN:CAA52273.1; PID:g437042

C:Genetics:

A:Gene: GBSS; waxy

A:Genome: nuclear

C:Function:

A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose produc

C:Superfamily: starch synthase

C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltra

F;1-78/Domain: transit peptide (amyloplast) #status predicted <NRP>

F;79-608/Product: ADPglucose-starch glucosyltransferase #status predicted <MAT>

Query Match 53.5%; Score 1481.5; DB 2; Length 608;

Best Local Similarity 55.0%; Pred. No. 6.4e-94;

Matches 299; Conservative 64; Mismatches 148; Indels 33; Gaps 9;

QY 2 LDIVMAAEVAPWSKTGGLGDTGGLPIELVKGRHVTIAPRYDQYADAWDSVVVDI- 60

Db 82 MNLIFVGAEGVPSKGTGLGDLGLPPAAARHVRVTVSPRYDQKQDAWDSVSVIEK 141

QY 61 MG---EKVRFHSIKGVHVRWIDHPWFLAKVWGKSGKLYGPRSGADYLDNHRKRALFC 117

Db 142 IGRIETVRFHFSKGVDRVFDHPMFLKGVKSGKLYGPRAGLDYQDNQLRFLSLC 201

QY 118 KAAIEARVLFP-----GP-GEDCVFVANDHSHALVPLLLKDEYQPKQKAKSVLA 169

Db 202 LAALEAPRVNLNSSKNFSGPYGEEVAFANDWHHTALLPCYLKAIYQPMGIYKHAKVAF 261

QY 170 IHNIAFGRMWEAEFKDITKLPAADFKLAFSDGYAKVYTEATPMDEEKPLLTGKYTKI 229

Db 262 IHNIAVQGRFAISDFPRNLNPKFKSFFIDGYEK-----PVAG---RKI 304

QY 230 NMLKGIITAAADKLVTVSPNYATEIAADAAGGVDELTVIRAKGIEGVINGMDIEWPKTD 289

Db 305 NNMKAGILESRLVITVSPYAAQEVISGVERGVELDNFIRKTIAGIINGMDVQWNPVD 364

QY 290 KFLSAPYDONSYYAGKAAKAEALQELGLPVPDTPAFIQRLEKQKGVDIILALPKI 349

Db 365 KYVIDHYDATTYMDAKPLLEKALQAEVGLPVDRNPLIGFIRGLEKQKGSDFVFAISQ- 423

starch (bacterial
probable starch sy
starch synthase (E
probable starch sy
starch synthase (E
glycogen synthase
glycogen synthase
starch synthase (E
starch synthase (E
soluble starch syn
hypothetical prote
glycogen synthase
glycogen synthase
glycogen (starch)
hypothetical prote

```

QY 350 LATPKVQIATILGTGKAAAYEKLVAIGTKYGRAGKGVKFSAPLAHMLTAGADFMVPSRF 409
DB 424 LVEHNVQIVILGTGKKKEKQIEHLEVLVDPDKARGVAKENVPLAHMITAGADFMVPSRF 483
QY 410 EPCGLIQLHAMHYGTPVAVSTGGVLDVTVEGVTGFHMGALNP--DKLDEADADALAIV 467
DB 484 EPCGLIQLHAMRYGTPVAVSTGGVLDVTVEGVTGFHMGALNP--DKLDEADADALAIV 543
QY 468 RRASEVFAGGRPPEMVAVNCISODLSWSKPAQKWEGLLEEVYKGVATKAEIKVPVA 527
DB 544 ARALGTATATAALREMLNCMAQDLSWKGPARMEKMLDLEV-TGSEPTGEGETIAPLAK 602
QY 528 EKIP 531
DB 603 ENVP 606

RESULT 2
YUPOY
starch synthase (EC 2.4.1.21) precursor - potato
N:Alternate names: starch synthase
C:Species: Solanum tuberosum (potato)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 02-Aug-2002
C:Accession: S16555; S24392; S26060; S26061
R:Van der Leij, F.R.; Visser, R.G.F.; Ponstein, A.S.; Jacobsen, E.; Feenstra, W.J.
Mol. Gen. Genet. 228, 240-248, 1991
A:Title: Sequence of the structural gene for granule-bound starch synthase of potato (Sc)
A:Reference number: S16555; MUID:91360072; PMID:1886609
A:Accession: S16555
A:Molecule type: DNA
A:Residues: 1-607 <LEI>
A:Cross-references: EMBL:X58453; NID:g21470; PIDN:CAA41359.1; PID:g21471
A>Note: the authors translated the codon AAC for residue 453 as Gly and GCT for residue
A:Accession: S24392
A:Molecule type: protein
A:Residues: 78-92, 'X', '94-98, 'XXX', 102, 'XX', 105-107 <LE2>
R:Rohde, W.; Becker, D.; Kull, B.; Salamini, F.
J. Genet. Breed. 44, 311-315, 1990
A:Title: Structural and functional analysis of two waxy gene promoters from potato.
A:Reference number: S26060
A:Accession: S26060
A:Molecule type: DNA
A:Residues: 1-43 <ROH1>
A:Cross-references: EMBL:X52416; NID:g21613; PIDN:CAA36667.1; PID:g21614
A:Experimental source: cv. Granola, clone G1
A:Accession: S26061
A:Molecule type: DNA
A:Residues: 1-43 <ROH2>
A:Cross-references: EMBL:X52417; NID:g21615; PIDN:CAA36668.1; PID:g21616
A:Experimental source: cv. Granola, clone G28
C:Genetics:
A:Gene: waxy
A:Genome: nuclear
A:Introns: 111/3; 138/3; 171/3; 201/3; 223/1; 256/3; 293/2; 374/3; 433/3; 497/3; 526/3;
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing e
A:Pathway: starch biosynthesis
C:Superfamily: starch synthase
C:Keywords: amyloplast; glycogen/starch biosynthesis; glucosyltransferase; hexosyltransf
F:1-77/Domain: transit peptide (amyloplast) #status predicted <INP>
F:78-607/Product: ADPglucose-starch glucosyltransferase #status experimental <MAT>

Query Match 52.6%; Score 1457.5; DB 1; Length 607;
Best Local Similarity 54.0%; Pred. No. 2.8e-92;
Matches 295; Conservative 67; Mismatches 143; Indels 41; Gaps 10;

QY 2 LDIWVAEAVPWSKTGGLGVTGCLPIELVKRHRVMTIAPRYDQYADADMTSVVVDI- 60
DB 81 MNLIFVGTVEGVPWSKTGGLGVTGCLPIELVKRHRVMTIAPRYDQYADADMTSVVVDI- 140
QY 61 MG--EKVRYFHSIKKGVHRVWIDHPWFLAKVWGTGSKLYGPRSGADYLDNHRKRALFC 117

```

```

DB 141 VGSIEIVRFFHCYKRCVDRVFDHPMFLEKLVWVGKTSKIYGPAGLDYLDNELRSLIC 200
QY 118 KAAIEAARYLPF-----GP-GECCVFAVNDKHSALVPLVKDETPQKQFTKAKSVLA 169
DB 201 QAALEAPKVLNLSNSSFSGPYGDEVLFITANDWHTALIPCYLKSMTQSRGIYLNKAVAF 260
QY 170 IHNIAFGQRMWEAFKDTIKPQAAFDKLAFCGAKYVYTEATPMEDEKPPPLGKTYKKI 229
DB 261 IHNIAFGQRFSTSDFFLLNLPDEFGRGSDFDICYEK-----PVKG---RKI 303
QY 230 NMLKGLIADKLVTVPSPNYATEIAADAAGGVDELDTVIRAKLEGIVNGMDIEWPKTD 289
DB 304 NMLKGLIADKLVTVPSPNYATEIAADAAGGVDELDTVIRAKLEGIVNGMDIEWPKTD 363
QY 290 KFLSAPYDQNSVYAGKAAKEALQAEGLDVPDTPAFLEAFIGLEEQKGVDDIILALPKI 349
DB 364 KYTDVKYDITVMDAKPPLLKEALQAAVAVPDKKIPKIPGIFGRLEEQKGVDDIILALPKI 423
QY 350 LATPKVQIATILGTGKAAAYEKLVAIGTKYGRAGKGVKFSAPLAHMLTAGADFMVPSRF 409
DB 424 IGL-DWQIVVLGTGKKEFEQEIQLLEVLYPNKAGVAKFNVPLAHMITAGADFMVPSRF 482
QY 410 EPCGLIQLHAMHYGTPVAVSTGGVLDVTVEGVTGFHMGALNP--DKLDEADADALAIV 467
DB 483 EPCGLIQLHAMRYGTPVAVSTGGVLDVTVEGVTGFHMGALNP--DKLDEADADALAIV 542
QY 468 RRASEVFAGGRPPEMVAVNCISODLSWSKPAQKWEGLLEEVYKGVATKAEIKVPVA 519
DB 543 ARALGTATATAALREMLNCMAQDLSWKGPARMEKMLDLEV-TGSEPTGEGETIAPLAK 601
QY 520 EEIKVP 525
DB 602 ENVPAT 607

RESULT 3
S61504
glycogen(starch) synthase (EC 2.4.1.11) isoform I precursor - garden pea
N:Alternate names: glycogen(starch) synthase
C:Species: Pisum sativum (garden pea)
C:Date: 20-Jul-1996 #sequence_revision 07-Feb-1997 #text_change 16-Aug-2002
C:Accession: S61504; S72372
R:Dry, J.; Smith, A.; Edwards, A.; Bhattacharyya, M.; Dunn, P.; Martin, C.
Plant J. 2, 193-202, 1992
A:Title: Characterization of cDNAs encoding two isoforms of granule-bound starch synt
A:Reference number: S61504; MUID:93251108; PMID:1302049
A:Accession: S61504
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-603 <DRY>
A:Cross-references: EMBL:X88789; NID:g887570; PIDN:CAA61268.1; PID:g887571
A:Accession: S72372
A:Molecule type: protein
A:Residues: 76-77, 'X', 79, 81-88 <DRW>
C:Superfamily: starch synthase
C:Keywords: glucosyltransferase; hexosyltransferase
F:1-75/Domain: signal sequence #status predicted <SIG>
F:76-603/Product: glycogen(starch) synthase isoform I #status experimental <MAT>

Query Match 51.1%; Score 1415.5; DB 2; Length 603;
Best Local Similarity 51.8%; Pred. No. 2.2e-89;
Matches 284; Conservative 79; Mismatches 140; Indels 45; Gaps 12;

QY 2 LDIWVAEAVPWSKTGGLGVTGCLPIELVKRHRVMTIAPRYDQYADADMTSVVVDI- 60
DB 77 MSLVFGVAGVPGWSKTGGLGVTGCLPIELVKRHRVMTIAPRYDQYADADMTSVVVDI- 136
QY 61 MGEK---VRYFHSIKKGVHRVWIDHPWFLAKVWGTGSKLYGPRSGADYLDNHRKRALFC 117
DB 137 VGDKTETVRFHCYKRGVDRVFDHPWFLAKVWGTGSKLYGPRSGADYLDNHRKRALFC 196
QY 118 KAAIEAARYLPF-----GP-GECCVFAVNDKHSALVPLVKDETPQKQFTKAKSVLA 169

```

Db 197 QAALEAPRVNLNLSKIFSGPYGEDIIVFVANDWHSALIPCLYSKMYKSLGNKAKVATC 256
 QY 170 IHNIATQGRWEEAFKPD---TKLPQAAEDKLFASDGYAKVYTEATPMEDEKPPPLTGKTY 226
 Db 257 IHNIATQGR---NAPSDFSLNLPDEFSSFDIDYKN-----PCBG--- 296
 QY 227 KKNLWKGITIAADKLVTVSPNYATEIAADAAGGVDELDIRAKGIEGIVNGMDTEWNP 286
 Db 297 KKNWKGITIAADKLVTVSPNYATEIAADAAGGVDELDIRAKGIEGIVNGMDTEWNP 286
 QY 287 KIDKELSPYDONSUYAGKAAAEALQAEGLPVDPTAPLFAFAGIEGIEGIVNGMDTEWNP 346
 Db 357 QTDRIYDHYNETTTEAKPLKGLQAEIGLPVDSIPPLIGFIEGIEGIVNGMDTEWNP 416
 QY 347 PKILATPKVQIALLGTGAAYEKLVNAIGTKYKGRAGKGVKFSAPLAHMLTAGADFMVLP 406
 Db 417 AK-FADENQVIVLGTGKIMEKQIEVLEEKYPGKAIGITKFNPSLAHMLTAGADFMVLP 475
 QY 407 SRFEPCGLIOLHAMHYGTVPVVASTGGLVDVTKVGTGFHMGALNP---DKLDEADADALA 464
 Db 476 SRFEPCGLVQLHAMHYGTVPVVASTGGLVDVTKVGTGFHMGALNP---DKLDEADADALA 464
 QY 465 ATVRASVFAAGRPYEMVANCISODLSWSKPAQKWEGLLEEV-----VYKGG--VATA 517
 Db 536 ATVRALKTYGTQAKQIILNMAQNFSSWKKPAKLEKALLNLEVTGNVAGIDGDEIAPL 595
 QY 518 KKEIKVP 525
 Db 596 AKENVATP 603

RESULT 4

T10906
 N:starch synthase (EC 2.4.1.21) - sweet potato
 C:Species: Ipomoea batatas (sweet potato)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002
 C:Accession: T10906
 R:Wang, S.J.; Yeh, K.W.; Tsai, C.Y.
 A:Reference number: 217212
 A:Accession: T10906
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-608 <WAN>
 A:Cross-references: EMBL:U44126; NID:gl172158; PID:gl172159
 A:Experimental source: cv. Tainong, tuberous root
 C:Genetics:
 A:Gene: SS67
 C:Function:
 A:Description: catalyzes the alpha-1,4-glucosylation of starch by ADPglucose producing a
 A:Pathway: starch biosynthesis
 C:Superfamily: starch synthase
 C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 51.0%; Score 1412.5; DB 2; Length 608;
 Best Local Similarity 53.5%; Pred. No. 3.5e-89;
 Matches 292; Conservative 61; Mismatches 152; Indels 41; Gaps 10;
 QY 2 LDIVMVAEAPWSPKSGGLGSDVTGGPLIELVKRHRVMTIAPDYQYADAWDTSVVVDI- 60
 Db 82 MNLVFGCEGPPCKTGGGLGDLVGLPAPLAARGHRVMTVCPRDYQYADAWDTSVVVDI- 60
 QY 61 MG---EKVRVFSHKKGVHVRWIDHPWFLAKVWGKSGKLYGPRSGADYLDNKHKRALFC 117
 Db 142 VGRDIEVRFHFKYKRGVDRVFDHPWFLAKVWGKSGKLYGPRSGADYLDNKHKRALFC 117
 QY 118 KAAIEAARVLPF-----GP-GEDCVFVANDWHSALVPVLLKDEYKQKGFYKAKSVLA 169
 Db 202 QAALEAPRVNLNLSKIFSGPYGEDIIVFVANDWHSALVPVLLKDEYKQKGFYKAKSVLA 169
 QY 170 IHNIATQGRWEEAFKPDTKLPQAAFDKLFASDGYAKVYTEATPMEDEKPPPLTGKTYK 229
 Db 257 IHNIATQGRWEEAFKPDTKLPQAAFDKLFASDGYAKVYTEATPMEDEKPPPLTGKTYK 229

Db 262 IHNIATQGRFAFSDFSLNLPDEYKGSFDFIDGYK-----PVKG---RKI 304
 QY 230 NMLKGGIIAADKLVTVSPNYATEIAADAAGGVDELDIRAKGIEGIVNGMDTEWNP 289
 Db 305 NMLKGGIIAADKLVTVSPNYATEIAADAAGGVDELDIRAKGIEGIVNGMDTEWNP 289
 QY 290 KFLSAPYDONSUYAGKAAAEALQAEGLPVDPTAPLFAFAGIEGIEGIVNGMDTEWNP 349
 Db 365 KYLAVKYDITVQAKPPLKKEALQAAVGLPVDNIPPLIGFIEGIEGIVNGMDTEWNP 424
 QY 350 LATPKVQIALLGTGAAYEKLVNAIGTKYKGRAGKGVKFSAPLAHMLTAGADFMVLP 409
 Db 425 ISM-DVQIILGTGKKEFEQIEQLEVMYDPKARGVAKFNVLHMHITAGADFMVLP 483
 QY 410 EPCGLIOLHAMHYGTVPVVASTGGLVDVTKVGTGFHMGALNP---DKLDEADADALA 467
 Db 484 EPCGLIOLHAMHYGTVPVVASTGGLVDVTKVGTGFHMGALNP---DKLDEADADALA 467
 QY 468 RRASEVFAAGRPYEMVANCISODLSWSKPAQKWEGLL-----FEVYKGGVATK 519
 Db 544 GRALATYGTAFTEMIKNMQSGLSKGPAKWEIVLLSGVAGSEPGVEGE-ETAPLAK 602
 QY 520 BEIKVP 525
 Db 603 ENVATP 608

RESULT 5

JQ0703
 N:glycogen(starch) synthase (EC 2.4.1.11) - rice
 C:Species: Oryza sativa (rice)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-2002
 C:Accession: JQ0703
 R:Wang, Z.Y.; Wu, Z.L.; Xing, Y.Y.; Zheng, F.G.; Guo, X.L.; Zhang, W.G.; Hong, M.M.
 A:Reference number: JQ0703; MUID:91016948; PMID:2216792
 A:Accession: JQ0703
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-609 <WAN>
 A:Cross-references: EMBL:X53694
 A:Experimental source: strain subsp. japonica Hengfeng
 C:Genetics:
 A:Gene: waxy
 A:Introns: 114/1; 141/1; 174/1; 204/1; 225/2; 259/1; 295/3; 377/1; 436/1; 500/1; 529/1
 C:Function:
 A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose produc
 C:Superfamily: starch synthase
 C:Keywords: chloroplast; glycogen/starch biosynthesis; glycosyltransferase; hexosyltr

Query Match 50.5%; Score 1398.5; DB 2; Length 609;
 Best Local Similarity 51.2%; Pred. No. 3.2e-88;
 Matches 280; Conservative 77; Mismatches 147; Indels 43; Gaps 9;
 QY 2 LDIVMVAEAPWSPKSGGLGSDVTGGPLIELVKRHRVMTIAPDYQYADAWDTSVVVDI- 60
 Db 83 MNLVFGCEGPPCKTGGGLGDLVGLPAPLAARGHRVMTVCPRDYQYADAWDTSVVVDI- 60
 QY 61 ---MGKVRVFSHKKGVHVRWIDHPWFLAKVWGKSGKLYGPRSGADYLDNKHKRALFC 117
 Db 143 VADRIEVRFFHFKYKRGVDRVFDHPWFLAKVWGKSGKLYGPRSGADYLDNKHKRALFC 117
 QY 118 KAAIEAARVLPF-----PFGP-GEDCVFVANDWHSALVPVLLKDEYKQKGFYKAKSVLA 169
 Db 203 QAALEAPRVNLNLSKIFSGPYGEDIIVFVANDWHSALVPVLLKDEYKQKGFYKAKSVLA 169
 QY 170 IHNIATQGRWEEAFKPDTKLPQAAFDKLFASDGYAKVYTEATPMEDEKPPPLTGKTYK 229
 Db 263 IHNIATQGRFAFEDYFELNLSERFSDFIDGY-----DTPVEG-----RKI 305
 QY 230 NMLKGGIIAADKLVTVSPNYATEIAADAAGGVDELDIRAKGIEGIVNGMDTEWNP 289

306	Db	: : :: : : :: : :	NNWKAGILEADRVLTSPYYAEELISGIARGCELDNIMRLTGITGVNGMDVSEWDP	SKD 365
290	Qy	KFLSAPVDQNSVYAGKAAAEALQAEGLPVDPTAPLFAF1GRLEEQKGVDIILAALPKI	349	
366	Db	: : : : :	KYITADYATTAATEAKALNKEALQAEAGLPVDRKIPLAF1GRLEEQKGPVMAAIIPEL	425
350	Qy	LATPKVQIATLGTCAAYEKLVAIGTKYKGRAGVVKFSAPLAHMLTAGADFM	LVP	SRF 409
426	Db	M-QEDVQIVLLGTGKKFKEKLLKSMEEKYPCGVRAVVKFNAPLAHLMAGADV	LAV	SRF 484
410	Qy	EPGLIQLHAWHYGTVPVVA	TGGTGLVDTVKSGVGFHMGALNPD--KLDEADADALA	ATV 467
485	Db	EPGLIQLQGMRYGTACACASTGGLVDTV1EGKTGFHMGRLSDGVKVP	EP	SDVKVKAATL 544
468	Qy	RRASEVAGGYPPEWANCISODLSWSPAKQWEGLLSEVYVKGK-----VATAK	518	
545	Db	KRAIKVGTPTAYEEMVRNMCNQDLSWKGP	AKN	ENVL--LGLGVAGSAPGIEGDEIAPLA 602
519	Qy	KEEIKVP 525		
603	Db	KENVAAP 609		

RESULT 6

S11481
glycogen(starch) synthase (EC 2.4.1.11) precursor - rice
N:Alternate names: starch synthase; waxy protein
C:Species: Oryza sativa (rice)
C:Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2002
C:Accession: S11481; S22519; S30485; PC2190; J02224
R:Wang, Z.Y.; Wu, Z.L.; Xing, Y.X.; Zheng, F.G.; Guo, X.L.; Zhang, W.G.; Hong, M.M.
Nucleic Acids Res. 18, 5898, 1990
A:Title: Nucleotide sequence of rice waxy gene.
A:Reference number: JQ0703; MUID:91016948; PMID:2216792
A:Accession: S11481
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-609 <WAX>
A:Cross-references: EMBL:X53694; NID:g577598; PIDN:CAA37732.1; PID:g577599
R:Okagaki, R.J.
Plant Mol. Biol. 19, 513-516, 1992
A:Title: Nucleotide sequence of a long cDNA from the rice waxy gene.
A:Reference number: S22519; MUID:92322986; PMID:1377969
A:Accession: S22519
A:Molecule type: mRNA
A:Residues: 1-609 <OKA>
A:Cross-references: EMBL:X62134; NID:g20402; PIDN:CAA44065.1; PID:g20403
R:Hirano, H.Y.; Sano, Y.
Plant Cell Physiol. 32, 989-997, 1991
A:Title: Molecular characterization of the waxy locus of rice (Oryza sativa).
A:Reference number: S30485
A:Accession: S30485
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-609 <HIR>
A:Cross-references: EMBL:X58228; NID:g20400; PIDN:CAA41186.1; PID:g20401
A:Accession: PC2190
A:Molecule type: protein
A:Residues: 78-113 <HIR>
A:Experimental source: leaf, cDNA POSLHC2120
C:Comment: this protein is involved in amylose synthesis in the rice endosperm.
C:Genetics:
A:Gene: waxy
A:Introns: 113/3; 140/3; 173/3; 203/3; 225/1; 258/3; 295/2; 376/3; 435/3; 499/3; 528/3;
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose producing
A:Pathway: starch biosynthesis
C:Superfamily: starch synthase
C:Keywords: amyloplast; chloroplast; glycogen/starch biosynthesis; glycosyltransferase;
F:1-77/Domain: transit peptide (amyloplast) #status predicted <TNP>
F:78-609/Product: glycogen (starch) synthase #status experimental <MAT>

Query Match	50.5%;	Score 1397.5;	DB 2;	Length 609;
Best Local Similarity	51.4%;	Pred. No. 3.3e-88;		
Matches	281;	Conservative	76;	Mismatches 147; Indels 43; Gaps 9;

QY	2	LDIVMAAEAVPASKTGGGLDVTGGGLPIELVKRGHVRMTIAPRYDQYADAWDTSVVVDI-	60
Db	83	MNVFVGAENAPNSKTGGDLVGLPPAMAAANGHRVWVTSRYDQYKDAWDTSVVAEIK	142
QY	61	---MGEKVRVPHSIKKGVHRVWIDHPWFLAKVAGKTSKLYGPRSGADYLDNHRKRALFC	117
Db	143	VADRYEKVRFFHCYKRGVDVRFIDHPSFLBKVMGKTGEKIGYDPTGVVDYKDNQMRSLLC	202
QY	118	KAATEAARVL----PRGP---GDCVCFVANDMHSALVPVLLKDEYQPKGQTFKAKSVLA	169
Db	203	QAALAEAPRLNANNPFYKGTGYGDDVVFVNCDAHTGTPLASVLYKNNYQPNGIYRNAKVAFC	262
QY	170	IHNIAFOGRMWEEAFKDTKILPQAAFDKLAFSDGYAKYVYTEATPMEEDEKPLTGKTYKKI	229
Db	263	IHNISYQGRFAFEDYPENLISERFSRSDFDIDG-----DTPVEG-----RKI	305
QY	230	NWLKGGIIAADKLVTPSPNATEIAADAAGGVELDTVIRAKIEGIVNGMDIEWNPKTD	289
Db	306	NMMKAGILEADRVLTVPFYAEELISGIARCELDNIMRLTGITGIVNGMDVSEMDPSKD	365
QY	290	KFLSAPYDQNSVYAGKAAAEALQAEILGLPVDTPAPLFAFIGRLEEBEOKGVDDIILALPKI	349
Db	366	KYITAKYDATTATIEAKALKEALQAEAGLPVDRKIPLIATFIGRLEEBEOKGPDVMAAATPEL	425
QY	350	LATPKVQIAILGTGKAAKEKLVNAIGTKYKGRAGVVKFSAPLAHMLTAGADFMLVPSRF	409
Db	426	M-QEDVQIVLLGTGKKFKPEKULKKEEYKIPGRVAVVKFNAPLAHLINAGADVLPVSRF	484
QY	410	EPCGLIQLHAMHYGTPVPVASTGGLVDTPKVEGVTFGHMGALNPD--KLDEADADALAAATV	467
Db	485	EPCGLIQLQGMRYGTPPCACASTGGLVDIVIEBKTGFHMGRLSVDCKVVEPSDVKKVAATL	544
QY	468	PRASEVFAGGRYPPEWVANCISQDLSWSKPAQKWEGLLEEVYVYKGG-----VATAK	518
Db	545	KRAIKVGTPTAYEEMVRNCMNODLSWKGPANKWENVL--LGLGVAGSAPGIEGDEIAPLA	602
QY	519	KEEKIVP 525	
Db	603	KENVAAP 609	

RESULT 7
YUBHY
glycogen(starch) synthase (EC 2.4.1.11) precursor - barley
N:Alternate names: starch synthase
C:Species: Hordeum vulgare (barley)
C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 02-Aug-2002
C:Accession: S01727; S01728
R:Rohde, W.; Becker, D.; Salamini, F.
Nucleic Acids Res. 16, 7185-7186, 1988
A:Title: Structural analysis of the waxy locus from Hordeum vulgare.
A:Reference number: S01727; MUID:88303345; PMID:2970062
A:Accession: S01727
A:Molecule type: DNA
A:Residues: 1-603 <ROH>
A:Cross-references: EMBL:X07931; NID:g19126; PIDN:CAA30755.1; PID:g295809
A:Accession: S01728
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-603 <NOH>
A:Cross-references: EMBL:X07932; NID:g19128; PIDN:CAA30756.1; PID:g19129
C:Genetics:
A:Gene: waxy
A:Introns: 106/3; 133/3; 166/3; 218/1; 251/3; 369/3; 429/3; 493/3; 522/3; 565/3
C:Function:
A:Description: catalyzes the alpha-1,4-glucosylation of starch by UDPglucose P
A:Pathway: starch biosynthesis
C:Superfamily: starch synthase
C:Keywords: amyloplast; glycogen/starch biosynthesis; glycosyltransferase; hexa